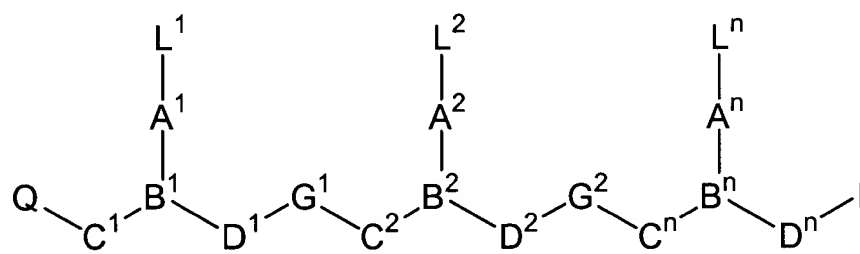


(ii) *Amendment To The Claims:*

1. (Currently Amended) A ~~non-nucleic acid~~ PNA probe of 10 to 30 subunits in length ~~having~~ comprising a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of: CTT-CAA-AGA-GGT-CCA-CGA (Seq. ID No. 1); AGG-GTT-CAA-CTG-TGT-GAC (Seq. ID No. 2); GAA-ACT-TCT-GAG-TGA-TGA (Seq. ID No. 3); CAG-TCA-TCG-CAG-AAA-ACT (Seq. ID No. 4); AGA-TTT-CAC-TGG-AAA-CGG (Seq. ID No. 5); GTT-ATG-GGA-AGG-TGA-TCC (Seq. ID No. 6); TCG-AGC-CGC-AGA-GTT-TAA (Seq. ID No. 7); CTA-TTT-AGC-GGG-CTT-GGA (Seq. ID No. 8); TAC-AAG-GGT-GTT-GCA-AAC (Seq. ID No. 9); CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT (Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC (Seq. ID No. 14); CAG-AAG-AGA-TTG-AAC-CTT (Seq. ID No. 15); GGC-ATA-GCA-CAT-AAC-ATG (Seq. ID No. 16); AAT-CGT-CAT-CGA-ATG-AAT (Seq. ID No. 17); CAT-TGA-ACA-GAA-TTG-AAT (Seq. ID No. 18); GTT-TTC-AGG-GGA-AGA-TAT (Seq. ID No. 19); TGT-GCG-CCC-TCA-ACT-AAC (Seq. ID No. 20); GAA-GCT-TCA-TTG-GGA-TGT (Seq. ID No. 21); CCA-ATA-AAA-GCT-ACA-TAG-A (Seq. ID No. 22); GAA-AAA-GTT-TCT-GAC-ATT-GC (Seq. ID No. 23); TAG-TTG-AAG-GGC-ACA-TCA (Seq. ID No. 24); CAC-AAA-TAA-GAT-TCT-AAG-AAT (Seq. ID No. 25); TCA-AAA-GAA-TGC-TTC-AAC-AC (Seq. ID No. 26); ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27); GCT-GTT-TTC-TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-AAG-AGG-TCC (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-AAG (Seq. ID No. 30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No. 31); TGT-GTA-TCA-ACT-CAC-GGA (Seq. ID No. 32); CCT-CAC-AAA-GTA-GAA-ACT (Seq. ID No. 33); GAA-AAA-GCA-GTT-ACT-GAG (Seq. ID No. 34); TAA-TAA-TTA-GAC-GGA-ATC-AT (Seq. ID No. 35); TTA-CAG-GGC-ATT-GAA-GCC (Seq. ID No. 36); CAG-TTA-TGA-AGC-AGT-CTC (Seq. ID No. 37); CAC-ACC-AGA-AAA-AGC-AGT (Seq. ID No. 38); AAG-GGT-AAA-CAC-TGT-GAG (Seq. ID No. 39); AGA-CAA-CGA-AAT-

ATC-TTC-ATG (Seq. ID No. 40); CTA-GCA-GTA-TGA-GGT-CAA (Seq. ID No. 41);  
 GCA-GAC-TTC-AGA-AAC-AGA (Seq. ID No. 42); GGC-CTC-AAA-GAC-GTT-  
 TAA (Seq. ID No. 43); GTG-AAA-GTT-CCA-AGT-GAA (Seq. ID No. 44); GAG-  
 TGC-TTT-GAA-GCC-TAC (Seq. ID No. 45); GAA-ACA-GCA-GAG-TTG-AAA  
 (Seq. ID No. 46); TGC-AGA-GAT-CAC-AAC-GTG (Seq. ID No. 47); ACA-AAG-  
 AAT-CAT-TCG-CAG (Seq. ID No. 48); AGT-GTT-AGA-AAA-CTG-CTC (Seq. ID  
 No. 49); CTG-TTC-AGA-GTA-ACA-TGA (Seq. ID No. 50); CCG-CTT-GGA-AAT-  
 ACT-ACA (Seq. ID No. 51); GAA-ATG-GAA-ATA-TCT-CCC-C (Seq. ID No. 52);  
 TCT-AGG-AGG-TCC-AAT-TAT (Seq. ID No. 53); GAA-TTC-CCA-AGT-GGA-TAT  
 (Seq. ID No. 54); CTG-TAG-GTT-TAG-ATG-AAG (Seq. ID No. 55); AAG-GAG-  
 TGT-TTC-CCA-ACT (Seq. ID No. 56); GGC-TTC-AAG-GCG-CTC-TAA (Seq. ID  
 No. 57); GCA-GAG-ACT-TCA-AAG-TGC (Seq. ID No. 58); CAC-ACA-CAC-GGT-  
 GGA-CCA (Seq. ID No. 59); CAA-AGG-GAA-TGT-TCC-ATT (Seq. ID No. 60);  
 CAC-ATA-GCA-GTG-TTT-GAG (Seq. ID No. 61); CTC-AAG-GCG-GTC-CAA-TTA  
 (Seq. ID No. 62); GAG-TCG-AAA-TGC-ACA-CAT (Seq. ID No. 63); TAC-CAA-  
 GAG-GAA-TGT-TGC (Seq. ID No. 64); ACG-GGA-TGC-AAT-ATA-AAA (Seq. ID  
 No. 65); TGA-AGA-TTC-TGC-ATA-CGG (Seq. ID No. 66); AAG-GTT-TGT-ACT-  
 GAC-AGA (Seq. ID No. 67); CTG-AAC-TAT-GGT-GAA-AAA (Seq. ID No. 68);  
 ACT-AAC-TGT-GCT-GAA-CAT (Seq. ID No. 69); CCC-ATG-AAT-GCG-AGA-TAG  
 (Seq. ID No. 70); AAC-TGA-ACG-CAC-AGA-TGA (Seq. ID No. 71); GGC-TAA-  
 TCT-TTG-AAA-TTG-AAA (Seq. ID No. 72); AGG-TGG-ATA-ATT-GGC-CCT (Seq.  
 ID No. 73); TGA-AGT-CCA-AAA-AAG-CAC (Seq. ID No. 74); CTT-AGA-CAT-  
 GGA-AAT-ATC (Seq. ID No. 75); AAG-GGG-TCT-AAC-TAA-TCA (Seq. ID No.  
 76); GTA-GTT-GTT-GAG-AAT-GAT (Seq. ID No. 77); AAC-TTC-CCA-GAA-CTA-  
 CAC (Seq. ID No. 78); ATT-CTT-GAA-ATG-GAA-CAC (Seq. ID No. 79); CTG-  
 TGA-TTG-CTG-ATT-TGG (Seq. ID No. 80); GTC-ATC-ACA-GGA-AAC-ATT (Seq.  
 ID No. 81); GAA-ATT-TCC-TGT-TGA-CAG-A (Seq. ID No. 82); GTT-TGA-AAG-  
 CTG-AAC-TAT-G (Seq. ID No. 83); TCC-TGT-AAT-GTT-CGA-CAG (Seq. ID No.  
 84); TCA-TAG-AAC-GCT-AGA-AAG (Seq. ID No. 85); ACC-TTT-CTT-TTG-ATG-  
 AAG-GA (Seq. ID No. 86); CAA-ATA-TCA-CAA-AAA-GAG-GG (Seq. ID No. 87);  
 GAG-TTG-AAT-AGA-GGC-AAC (Seq. ID No. 88); GGC-CAA-ATG-TAG-AAA-

AGG (Seq. ID No. 89); GCG-TTC-AAC-TCA-AGG-TGT (Seq. ID No. 90); TGT-CCT-TTA-GAC-AGA-GCA (Seq. ID No. 91); TGA-GAC-CAA-ATG-TAC-AAA-AG (Seq. ID No. 92); GAA-TAC-TGA-GTA-AGT-TCT-TTG (Seq. ID No. 93); AAC-TGC-ACA-AAT-AGG-GTG (Seq. ID No. 94); TGG-AGA-CAC-TGT-GTT-TGT (Seq. ID No. 95); CCA-GTT-GGA-GAT-TTC-AAT (Seq. ID No. 96); GAA-GCC-TGC-CAG-TGG-ATA (Seq. ID No. 97); TAC-AGC-ATT-CTG-GAA-ACC (Seq. ID No. 98); CCA-GAC-ACT-GCG-TAG-TGA (Seq. ID No. 99); ATA-TAA-TGC-TAG-AGG-GAG (Seq. ID No. 100); AAA-AAC-AAG-ACA-AAC-TCG (Seq. ID No. 101); ATT-TCA-GCT-GAC-TAA-ACA (Seq. ID No. 102); AAC-GAA-TTA-TGG-TCA-CAT (Seq. ID No. 103); GGT-GAC-GAC-TGA-GTT-TAA (Seq. ID No. 104); TTT-GGA-CCA-CTC-TGT-GGC (Seq. ID No. 105); AAC-GGG-ATA-ACT-GCA-CCT (Seq. ID No. 106); TTT-GTG-GTT-TGT-GGT-GGA (Seq. ID No. 107); AGG-GAA-TAG-CTT-CAT-AGA (Seq. ID No. 108); ATC-ACG-AAG-AAG-GTT-CTG (Seq. ID No. 109); CCG-AAG-ATG-TCT-TTG-GAA (Seq. ID No. 110); AAA-GAG-GTC-TAC-ATG-TCC (Seq. ID No. 111); TTC-CCG-TAA-CAA-CTA-TGC (Seq. ID No. 112); TCC-CGT-AAC-AAC-TAG-GCA (Seq. ID No. 113); AAA-AGG-AGT-GAT-CCA-ACC (Seq. ID No. 114); TCC-CTT-TGG-TAG-AGC-AGG (Seq. ID No. 115); ATT-TGA-GAT-GTG-TGT-ACT-CA (Seq. ID No. 116); GCA-CTT-ACC-GGC-CTA-AG (Seq. ID No. 117) and CTC-AGA-AAC-TTA-CTC-GTG (Seq. ID No. 118) wherein said PNA probe has the formula:



wherein,

n is at least 2,

each of L<sup>1</sup>-L<sup>n</sup> is independently selected from the group consisting of hydrogen,

hydroxy, (C<sub>1</sub>-C<sub>4</sub>)alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of  $C^1-C^n$  is  $(CR^6R^7)_y$ , where  $R^6$  is hydrogen and  $R^7$  is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or  $R^6$  and  $R^7$  are independently selected from the group consisting of hydrogen,  $(C_2-C_6)$ alkyl, aryl, aralkyl, heteroaryl, hydroxy,  $(C_1-C_6)$ alkoxy,  $(C_1-C_6)$ alkylthio,  $NR^3R^4$  and  $SR^5$ , where  $R^3$  and  $R^4$  are as defined above, and  $R^5$  is hydrogen,  $(C_1-C_6)$ alkyl, hydroxy-, alkoxy-, or alkylthio- substituted  $(C_1-C_6)$ alkyl, or  $R^6$  and  $R^7$  taken together complete an alicyclic or heterocyclic system;

each of  $D^1-D^n$  is  $(CR^6R^7)_z$ , where  $R^6$  and  $R^7$  are as defined above;

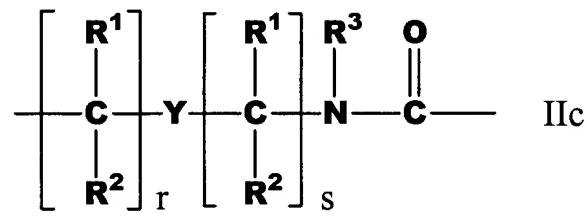
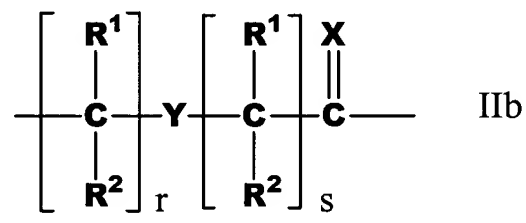
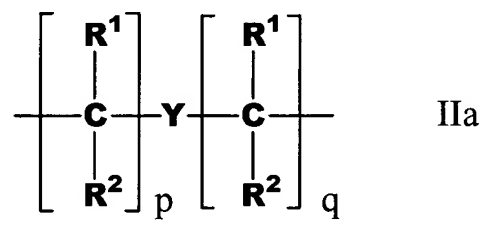
each of  $y$  and  $z$  is zero or an integer from 1 to 10, the sum  $y+z$  being greater than 2 but not more than 10;

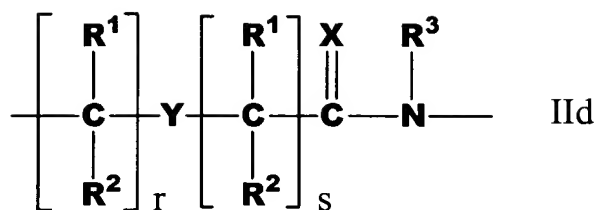
each of  $G^1-G^{n-1}$  is  $-NR^3CO-$ ,  $-NR^3CS-$ ,  $-NR^3SO-$  or  $-NR^3SO_2-$ , in either orientation, where  $R^3$  is as defined above;

each of  $A^1-A^n$  and  $B^1-B^n$  are selected such that:

(a)  $A$  is a group of the formula (IIa), (IIb), (IIc), or (IIId), and  $B$  is  $N$  or  $R^3N^+$ ; or

(b)  $A$  is a group of formula (IIId) and  $B$  is  $CH$ ;





where:

X is O, S, Se, NR<sup>3</sup>, CH<sub>2</sub> or C(CH<sub>3</sub>)<sub>2</sub>;

Y is a single bond, O, S or NR<sup>4</sup>;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R<sup>1</sup> and R<sup>2</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R<sup>3</sup> and R<sup>4</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is -CO<sub>2</sub>H, -CONR'R'', -SO<sub>3</sub>H or -SO<sub>2</sub>NR'R'' or an activated derivative of -CO<sub>2</sub>H or -SO<sub>3</sub>H; and

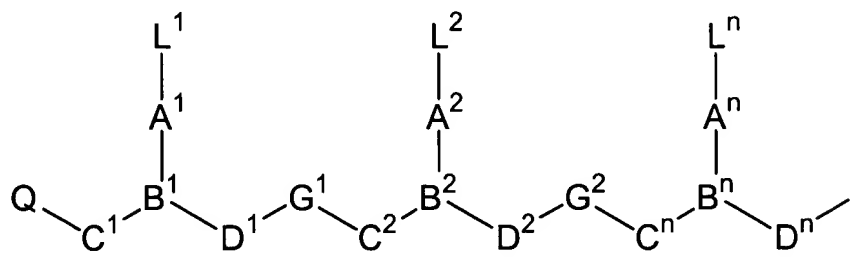
I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.

2. (Original) The probe of claim 1, wherein the probing nucleobase sequence is exactly as represented in the claim.

(Claims 3-9 Canceled)

10. (Currently Amended) A probe set comprising at least thirteen ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length and which is suitable for detecting,

identifying or enumerating human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18 in a sample wherein said PNA probes have the formula:



wherein,

n is at least 2,

each of L<sup>1</sup>-L<sup>n</sup> is independently selected from the group consisting of hydrogen, hydroxy, (C<sub>1</sub>-C<sub>4</sub>)alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C<sup>1</sup>-C<sup>n</sup> is (CR<sup>6</sup>R<sup>7</sup>)<sub>y</sub> where R<sup>6</sup> is hydrogen and R<sup>7</sup> is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R<sup>6</sup> and R<sup>7</sup> are independently selected from the group consisting of hydrogen, (C<sub>2</sub>-C<sub>6</sub>)alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C<sub>1</sub>-C<sub>6</sub>)alkoxy, (C<sub>1</sub>-C<sub>6</sub>)alkylthio, NR<sup>3</sup>R<sup>4</sup> and SR<sup>5</sup>, where R<sup>3</sup> and R<sup>4</sup> are as defined above, and R<sup>5</sup> is hydrogen, (C<sub>1</sub>-C<sub>6</sub>)alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C<sub>1</sub>-C<sub>6</sub>)alkyl, or R<sup>6</sup> and R<sup>7</sup> taken together complete an alicyclic or heterocyclic system;

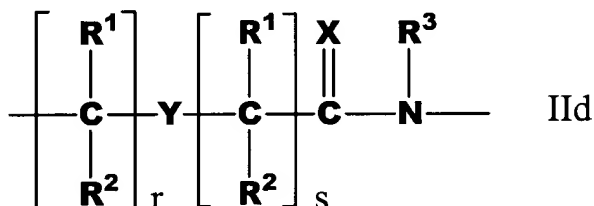
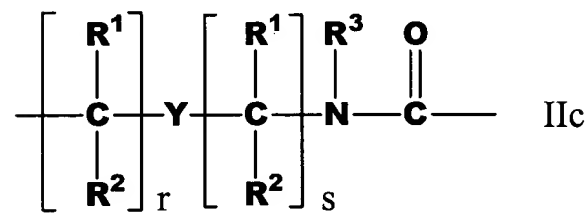
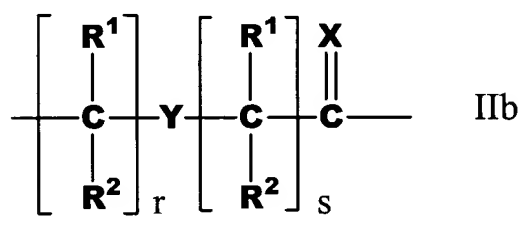
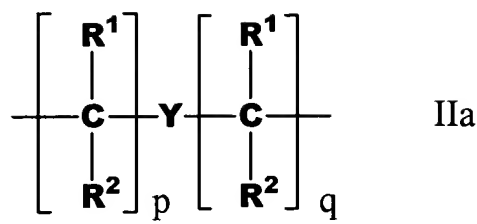
each of D<sup>1</sup>-D<sup>n</sup> is (CR<sup>6</sup>R<sup>7</sup>)<sub>z</sub> where R<sup>6</sup> and R<sup>7</sup> are as defined above;

each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

each of G<sup>1</sup>-G<sup>n-1</sup> is -NR<sup>3</sup>CO-, -NR<sup>3</sup>CS-, -NR<sup>3</sup>SO- or -NR<sup>3</sup>SO<sub>2</sub>-, in either orientation, where R<sup>3</sup> is as defined above;

each of A<sup>1</sup>-A<sup>n</sup> and B<sup>1</sup>-B<sup>n</sup> are selected such that:

- (a) A is a group of the formula (IIa), (IIb), (IIc), or (IId), and B is N or R<sup>3</sup>N<sup>+</sup>; or
- (b) A is a group of formula (IId) and B is CH;



where:

X is O, S, Se, NR<sup>3</sup>, CH<sub>2</sub>, or C(CH<sub>3</sub>)<sub>2</sub>;

Y is a single bond, O, S or NR<sup>4</sup>;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R<sup>1</sup> and R<sup>2</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R<sup>3</sup> and R<sup>4</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is  $-\text{CO}_2\text{H}$ ,  $-\text{CONR}'\text{R}''$ ,  $-\text{SO}_3\text{H}$  or  $-\text{SO}_2\text{NR}'\text{R}''$  or an activated derivative of  $-\text{CO}_2\text{H}$  or  $-\text{SO}_3\text{H}$ ; and

I is  $-\text{NHR}'''\text{R}''''$  or  $-\text{NR}'''\text{C}(\text{O})\text{R}''''$ , where  $\text{R}'$ ,  $\text{R}''$ ,  $\text{R}'''$  and  $\text{R}''''$  are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.

11. (Currently Amended) The probe set of claim 10, wherein:

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome X ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

CTT-CAA-AGA-GGT-CCA-CGA (Seq. ID No. 1); AGG-GTT-CAA-CTG-TGT-GAC (Seq. ID No. 2); GAA-ACT-TCT-GAG-TGA-TGA (Seq. ID No. 3); CAG-TCA-TCG-CAG-AAA-ACT (Seq. ID No. 4); AGA-TTT-CAC-TGG-AAA-CGG (Seq. ID No. 5); GTT-ATG-GGA-AGG-TGA-TCC (Seq. ID No. 6); TCG-AGC-CGC-AGA-GTT-TAA (Seq. ID No. 7); CTA-TTT-AGC-GGG-CTT-GGA (Seq. ID No. 8) and TAC-AAG-GGT-GTT-GCA-AAC (Seq. ID No. 9);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome Y ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT (Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC (Seq. ID No. 14); CAG-AAG-AGA-TTG-AAC-CTT (Seq. ID No. 15) and GGC-ATA-GCA-CAT-AAC-ATG (Seq. ID No. 16);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome 1 ~~have~~ comprise a probing nucleobase sequence, at least a



portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

AAT-CGT-CAT-CGA-ATG-AAT (Seq. ID No. 17) and CAT-TGA-ACA-GAA-TTG-AAT (Seq. ID No. 18);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome 2 ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

GTT-TTC-AGG-GGA-AGA-TAT (Seq. ID No. 19); TGT-GCG-CCC-TCA-ACT-AAC (Seq. ID No. 20); GAA-GCT-TCA-TTG-GGA-TGT (Seq. ID No. 21); CCA-ATA-AAA-GCT-ACA-TAG-A (Seq. ID No. 22); GAA-AAA-GTT-TCT-GAC-ATT-GC (Seq. ID No. 23); TAG-TTG-AAG-GGC-ACA-TCA (Seq. ID No. 24); CAC-AAA-TAA-GAT-TCT-AAG-AAT (Seq. ID No. 25) and TCA-AAA-GAA-TGC-TTC-AAC-AC (Seq. ID No. 26);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome 3 ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27); GCT-GTT-TTC-TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-AAG-AGG-TCC (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-AAG (Seq. ID No. 30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No. 31); TGT-GTA-TCA-ACT-CAC-GGA (Seq. ID No. 32); CCT-CAC-AAA-GTA-GAA-ACT (Seq. ID No. 33); GAA-AAA-GCA-GTT-ACT-GAG (Seq. ID No. 34); TAA-TAA-TTA-GAC-GGA-ATC-AT (Seq. ID No. 35); TTA-CAG-GGC-ATT-GAA-GCC (Seq. ID No. 36); CAG-TTA-TGA-AGC-AGT-CTC (Seq. ID No. 37); CAC-ACC-AGA-AAA-AGC-AGT (Seq. ID No. 38); AAG-GGT-AAA-CAC-TGT-GAG (Seq. ID No. 39); AGA-CAA-CGA-AAT-ATC-TTC-ATG (Seq. ID No. 40); CTA-GCA-GTA-TGA-GGT-CAA (Seq. ID No. 41); GCA-GAC-TTC-AGA-AAC-AGA (Seq. ID No. 42); GGC-CTC-AAA-GAC-GTT-TAA (Seq. ID No. 43); GTG-AAA-GTT-CCA-AGT-GAA (Seq. ID No. 44); GAG-TGC-TTT-

GAA-GCC-TAC (Seq. ID No. 45); GAA-ACA-GCA-GAG-TTG-AAA (Seq. ID No. 46); TGC-AGA-GAT-CAC-AAC-GTG (Seq. ID No. 47); ACA-AAG-AAT-CAT-TCG-CAG (Seq. ID No. 48); and AGT-GTT-AGA-AAA-CTG-CTC (Seq. ID No. 49);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome 6 ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

CTG-TTC-AGA-GTA-ACA-TGA (Seq. ID No. 50); CCG-CTT-GGA-AAT-ACT-ACA (Seq. ID No. 51); GAA-ATG-GAA-ATA-TCT-CCC-C (Seq. ID No. 52); TCT-AGG-AGG-TCC-AAT-TAT (Seq. ID No. 53); GAA-TTC-CCA-AGT-GGA-TAT (Seq. ID No. 54); CTG-TAG-GTT-TAG-ATG-AAG (Seq. ID No. 55); AAG-GAG-TGT-TTC-CCA-ACT (Seq. ID No. 56); GGC-TTC-AAG-GCG-CTC-TAA (Seq. ID No. 57); GCA-GAG-ACT-TCA-AAG-TGC (Seq. ID No. 58); CAC-ACA-CAC-GGT-GGA-CCA (Seq. ID No. 59); CAA-AGG-GAA-TGT-TCC-ATT (Seq. ID No. 60); CAC-ATA-GCA-GTG-TTT-GAG (Seq. ID No. 61); CTC-AAG-GCG-GTC-CAA-TTA (Seq. ID No. 62); GAG-TCG-AAA-TGC-ACA-CAT (Seq. ID No. 63) and TAC-CAA-GAG-GAA-TGT-TGC (Seq. ID No. 64);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome 8 ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

ACG-GGA-TGC-AAT-ATA-AAA (Seq. ID No. 65); TGA-AGA-TTC-TGC-ATA-CGG (Seq. ID No. 66); AAG-GTT-TGT-ACT-GAC-AGA (Seq. ID No. 67); CTG-AAC-TAT-GGT-GAA-AAA (Seq. ID No. 68); ACT-AAC-TGT-GCT-GAA-CAT (Seq. ID No. 69) and CCC-ATG-AAT-GCG-AGA-TAG (Seq. ID No. 70);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome 10 ~~have~~ comprise a probing nucleobase sequence, at least

a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

AAC-TGA-ACG-CAC-AGA-TGA (Seq. ID No. 71); GGC-TAA-TCT-TTG-AAA-TTG-AAA (Seq. ID No. 72); AGG-TGG-ATA-ATT-GGC-CCT (Seq. ID No. 73); TGA-AGT-CCA-AAA-AAG-CAC (Seq. ID No. 74); CTT-AGA-CAT-GGA-AAT-ATC (Seq. ID No. 75); AAG-GGG-TCT-AAC-TAA-TCA (Seq. ID No. 76) and GTA-GTT-GTT-GAG-AAT-GAT (Seq. ID No. 77);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome 11 ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

AAC-TTC-CCA-GAA-CTA-CAC (Seq. ID No. 78); ATT-CTT-GAA-ATG-GAA-CAC (Seq. ID No. 79); CTG-TGA-TTG-CTG-ATT-TGG (Seq. ID No. 80); GTC-ATC-ACA-GGA-AAC-ATT (Seq. ID No. 81); GAA-ATT-TCC-TGT-TGA-CAG-A (Seq. ID No. 82) and GTT-TGA-AAG-CTG-AAC-TAT-G (Seq. ID No. 83);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome 12 ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

TCC-TGT-AAT-GTT-CGA-CAG (Seq. ID No. 84); TCA-TAG-AAC-GCT-AGA-AAG (Seq. ID No. 85); ACC-TTT-CTT-TTG-ATG-AAG-GA (Seq. ID No. 86); CAA-ATA-TCA-CAA-AAA-GAG-GG (Seq. ID No. 87); GAG-TTG-AAT-AGA-GGC-AAC (Seq. ID No. 88); GGC-CAA-ATG-TAG-AAA-AGG (Seq. ID No. 89); GCG-TTC-AAC-TCA-AGG-TGT (Seq. ID No. 90); TGT-CCT-TTA-GAC-AGA-GCA (Seq. ID No. 91); TGA-GAC-CAA-ATG-TAC-AAA-AG (Seq. ID No. 92); GAA-TAC-TGA-GTA-AGT-TCT-TTG (Seq. ID No. 93); AAC-TGC-ACA-AAT-AGG-GTG (Seq. ID No. 94); TGG-AGA-CAC-TGT-GTT-TGT (Seq. ID No. 95) and CCA-GTT-GGA-GAT-TTC-AAT (Seq. ID No. 96);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome 16 ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

GAA-GCC-TGC-CAG-TGG-ATA (Seq. ID No. 97); TAC-AGC-ATT-CTG-GAA-ACC (Seq. ID No. 98); CCA-GAC-ACT-GCG-TAG-TGA (Seq. ID No. 99); ATA-TAA-TGC-TAG-AGG-GAG (Seq. ID No. 100) and AAA-AAC-AAG-ACA-AAC-TCG (Seq. ID No. 101);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome 17 ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

ATT-TCA-GCT-GAC-TAA-ACA (Seq. ID No. 102); AAC-GAA-TTA-TGG-TCA-CAT (Seq. ID No. 103); GGT-GAC-GAC-TGA-GTT-TAA (Seq. ID No. 104); TTT-GGA-CCA-CTC-TGT-GGC (Seq. ID No. 105); AAC-GGG-ATA-ACT-GCA-CCT (Seq. ID No. 106); TTT-GTG-GTT-TGT-GGT-GGA (Seq. ID No. 107); AGG-GAA-TAG-CTT-CAT-AGA (Seq. ID No. 108); ATC-ACG-AAG-AAG-GTT-CTG (Seq. ID No. 109); CCG-AAG-ATG-TCT-TTG-GAA (Seq. ID No. 110) and AAA-GAG-GTC-TAC-ATG-TCC (Seq. ID No. 111);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome 18 ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

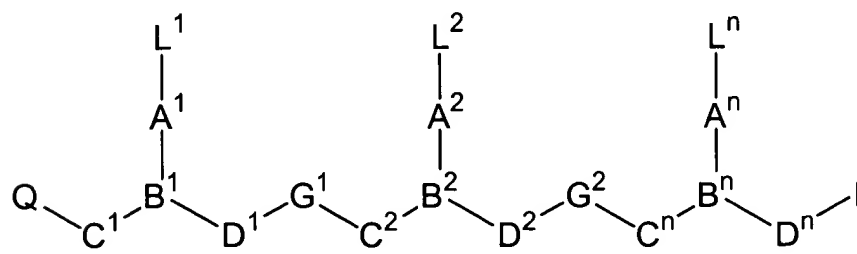
TTC-CCG-TAA-CAA-CTA-TGC (Seq. ID No. 112); TCC-CGT-AAC-AAC-TAG-GCA (Seq. ID No. 113); AAA-AGG-AGT-GAT-CCA-ACC (Seq. ID No. 114); TCC-CTT-TGG-TAG-AGC-AGG (Seq. ID No. 115); ATT-TGA-GAT-GTG-TGT-ACT-CA (Seq. ID No. 116); GCA-CTT-ACC-GGC-CTA-AG (Seq. ID No. 117) and CTC-AGA-AAC-TTA-CTC-GTG (Seq. ID No. 118).

12. (Original) The probe set of claim 11, wherein the probing nucleobase sequence of the probes of the set are exactly as represented in the claim.

(Claims 13-28 Canceled)

29. (Currently Amended) A probe set comprising ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length suitable for detecting the presence, absence or number of human chromosome 3 in a sample wherein the probing nucleobase sequence of at least one probe comprises a segment, at least a portion of which is, at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27); GCT-GTT-TTC-TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-AAG-AGG-TCC (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-AAG (Seq. ID No. 30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No. 31); TGT-GTA-TCA-ACT-CAC-GGA (Seq. ID No. 32); CCT-CAC-AAA-GTA-GAA-ACT (Seq. ID No. 33); GAA-AAA-GCA-GTT-ACT-GAG (Seq. ID No. 34); TAA-TAA-TTA-GAC-GGA-ATC-AT (Seq. ID No. 35); TTA-CAG-GGC-ATT-GAA-GCC (Seq. ID No. 36); CAG-TTA-TGA-AGC-AGT-CTC (Seq. ID No. 37); CAC-ACC-AGA-AAA-AGC-AGT (Seq. ID No. 38); AAG-GGT-AAA-CAC-TGT-GAG (Seq. ID No. 39); AGA-CAA-CGA-AAT-ATC-TTC-ATG (Seq. ID No. 40); CTA-GCA-GTA-TGA-GGT-CAA (Seq. ID No. 41); GCA-GAC-TTC-AGA-AAC-AGA (Seq. ID No. 42); GGC-CTC-AAA-GAC-GTT-TAA (Seq. ID No. 43); GTG-AAA-GTT-CCA-AGT-GAA (Seq. ID No. 44); GAG-TGC-TTT-GAA-GCC-TAC (Seq. ID No. 45); GAA-ACA-GCA-GAG-TTG-AAA (Seq. ID No. 46); TGC-AGA-GAT-CAC-AAC-GTG (Seq. ID No. 47); ACA-AAG-AAT-CAT-TCG-CAG (Seq. ID No. 48); and AGT-GTT-AGA-AAA-CTG-CTC (Seq. ID No. 49) wherein said PNA probes have the formula:



wherein,

n is at least 2,

each of L<sup>1</sup>-L<sup>n</sup> is independently selected from the group consisting of hydrogen, hydroxy, (C<sub>1</sub>-C<sub>4</sub>)alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C<sup>1</sup>-C<sup>n</sup> is (CR<sup>6</sup>R<sup>7</sup>)<sub>y</sub>, where R<sup>6</sup> is hydrogen and R<sup>7</sup> is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R<sup>6</sup> and R<sup>7</sup> are independently selected from the group consisting of hydrogen, (C<sub>2</sub>-C<sub>6</sub>)alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C<sub>1</sub>-C<sub>6</sub>)alkoxy, (C<sub>1</sub>-C<sub>6</sub>)alkylthio, NR<sup>3</sup>R<sup>4</sup> and SR<sup>5</sup>, where R<sup>3</sup> and R<sup>4</sup> are as defined above, and R<sup>5</sup> is hydrogen, (C<sub>1</sub>-C<sub>6</sub>)alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C<sub>1</sub>-C<sub>6</sub>)alkyl, or R<sup>6</sup> and R<sup>7</sup> taken together complete an alicyclic or heterocyclic system;

each of D<sup>1</sup>-D<sup>n</sup> is (CR<sup>6</sup>R<sup>7</sup>)<sub>z</sub>, where R<sup>6</sup> and R<sup>7</sup> are as defined above;

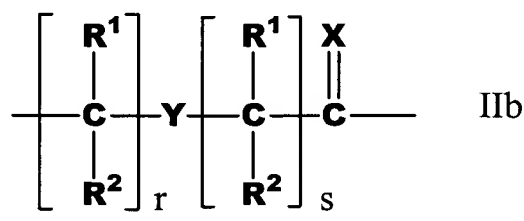
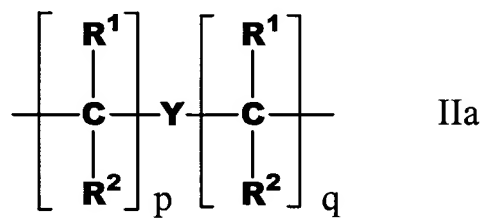
each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

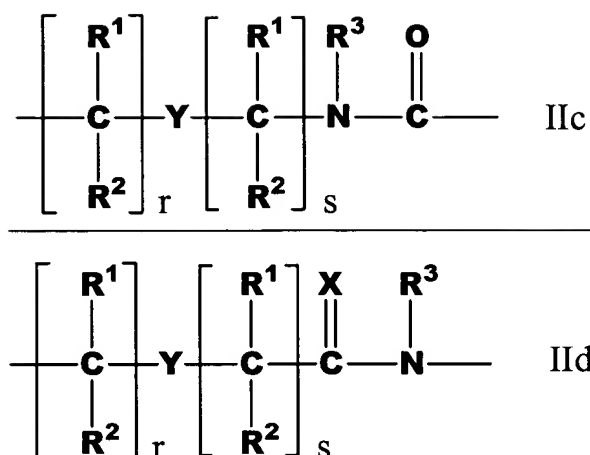
each of G<sup>1</sup>-G<sup>n-1</sup> is -NR<sup>3</sup>CO-, -NR<sup>3</sup>CS-, -NR<sup>3</sup>SO- or -NR<sup>3</sup>SO<sub>2</sub>-, in either orientation, where R<sup>3</sup> is as defined above;

each of A<sup>1</sup>-A<sup>n</sup> and B<sup>1</sup>-B<sup>n</sup> are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (IId), and B is N or R<sup>3</sup>N<sup>+</sup>; or

(b) A is a group of formula (IId) and B is CH<sub>3</sub>;





where:

X is O, S, Se, NR<sup>3</sup>, CH<sub>2</sub> or C(CH<sub>3</sub>)<sub>2</sub>;

Y is a single bond, O, S or NR<sup>4</sup>;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R<sup>1</sup> and R<sup>2</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R<sup>3</sup> and R<sup>4</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy, alkoxy, alkylthio and amino;

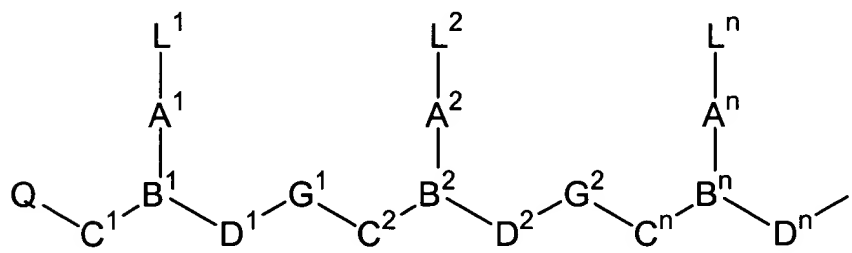
Q is -CO<sub>2</sub>H, -CONR'R'', -SO<sub>3</sub>H or -SO<sub>2</sub>NR'R'' or an activated derivative of -CO<sub>2</sub>H or -SO<sub>3</sub>H; and

I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.;

(Claim 30 Canceled)

31. (Currently Amended) A probe set comprising ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length suitable for detecting the presence, absence or number of human chromosome 8 in a sample wherein the probing nucleobase sequence of at least one probe comprises a segment, at least a portion of which is, at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

ACG-GGA-TGC-AAT-ATA-AAA (Seq. ID No. 65); TGA-AGA-TTC-TGC-ATA-CGG (Seq. ID No. 66); AAG-GTT-TGT-ACT-GAC-AGA (Seq. ID No. 67); CTG-AAC-TAT-GGT-GAA-AAA (Seq. ID No. 68); ACT-AAC-TGT-GCT-GAA-CAT (Seq. ID No. 69) and CCC-ATG-AAT-GCG-AGA-TAG (Seq. ID No. 70) wherein said PNA probes have the formula:



wherein,

n is at least 2,

each of  $L^1$ - $L^n$  is independently selected from the group consisting of hydrogen, hydroxy,  $(C_1-C_4)$ alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of  $C^1$ - $C^n$  is  $(CR^6R^7)_y$  where  $R^6$  is hydrogen and  $R^7$  is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or  $R^6$  and  $R^7$  are independently selected from the group consisting of hydrogen,  $(C_2-C_6)$ alkyl, aryl, aralkyl, heteroaryl, hydroxy,  $(C_1-C_6)$ alkoxy,  $(C_1-C_6)$ alkylthio,  $NR^3R^4$  and  $SR^5$ , where  $R^3$  and  $R^4$  are as defined above, and  $R^5$  is hydrogen,  $(C_1-C_6)$ alkyl, hydroxy-, alkoxy-, or alkylthio- substituted  $(C_1-C_6)$ alkyl, or  $R^6$  and  $R^7$  taken together complete an alicyclic or heterocyclic system;

each of  $D^1$ - $D^n$  is  $(CR^6R^7)_z$  where  $R^6$  and  $R^7$  are as defined above;



each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

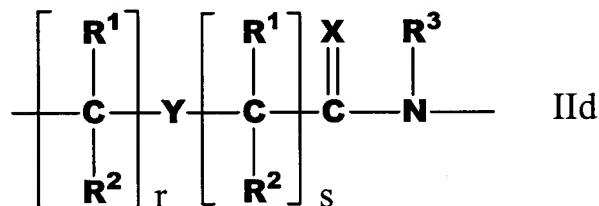
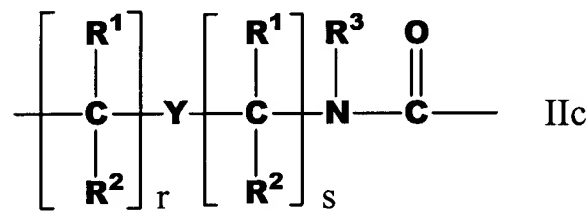
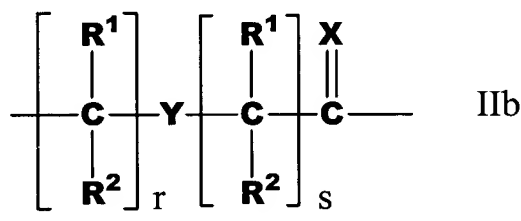
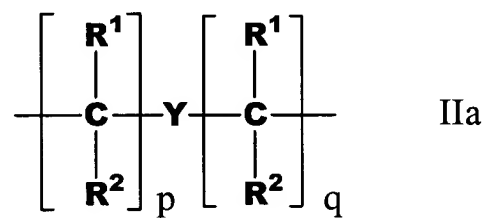
each of  $G^1$ - $G^{n-1}$  is  $-\text{NR}^3\text{CO}-$ ,  $-\text{NR}^3\text{CS}-$ ,  $-\text{NR}^3\text{SO}-$  or  $-\text{NR}^3\text{SO}_2-$ , in either orientation,

where  $\text{R}^3$  is as defined above;

each of  $\text{A}^1$ - $\text{A}^n$  and  $\text{B}^1$ - $\text{B}^n$  are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (IIId), and B is N or  $\text{R}^3\text{N}^+$ ; or

(b) A is a group of formula (IIId) and B is  $\text{CH}_2$ ;



where:

X is O, S, Se,  $\text{NR}^3$ ,  $\text{CH}_2$  or  $\text{C}(\text{CH}_3)_2$ ;

Y is a single bond, O, S or  $\text{NR}^4$ ;

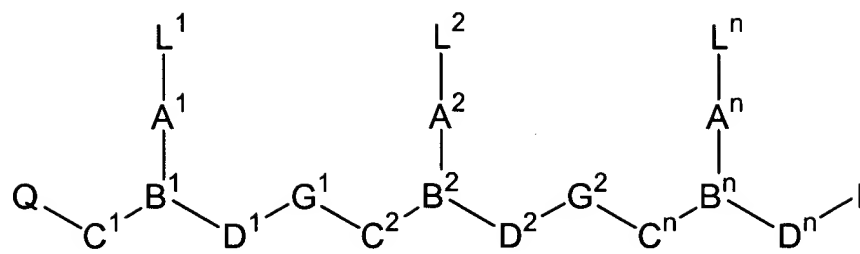
each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;  
each R<sup>1</sup> and R<sup>2</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and  
each R<sup>3</sup> and R<sup>4</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy, alkoxy, alkylthio and amino;  
Q is -CO<sub>2</sub>H, -CONR'R'', -SO<sub>3</sub>H or -SO<sub>2</sub>NR'R'' or an activated derivative of -CO<sub>2</sub>H or -SO<sub>3</sub>H; and  
I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.;

(Claim 32 canceled)

33. (Currently Amended) A probe set comprising ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length suitable for detecting the presence, absence or number of human chromosome 11 in a sample wherein the probing nucleobase sequence of at least one probe comprises a segment, at least a portion of which is, at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

AAC-TTC-CCA-GAA-CTA-CAC (Seq. ID No. 78); ATT-CTT-GAA-ATG-GAA-CAC (Seq. ID No. 79); CTG-TGA-TTG-CTG-ATT-TGG (Seq. ID No. 80); GTC-ATC-ACA-GGA-AAC-ATT (Seq. ID No. 81); GAA-ATT-TCC-TGT-TGA-CAG-A (Seq. ID No. 82) and GTT-TGA-AAG-CTG-AAC-TAT-G (Seq. ID No. 83) wherein said PNA probes have the formula:



wherein,

n is at least 2,

each of  $L^1$ - $L^n$  is independently selected from the group consisting of hydrogen, hydroxy,  $(C_1-C_4)$ alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of  $C^1$ - $C^n$  is  $(CR^6R^7)_y$  where  $R^6$  is hydrogen and  $R^7$  is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or  $R^6$  and  $R^7$  are independently selected from the group consisting of hydrogen,  $(C_2-C_6)$ alkyl, aryl, aralkyl, heteroaryl, hydroxy,  $(C_1-C_6)$ alkoxy,  $(C_1-C_6)$ alkylthio,  $NR^3R^4$  and  $SR^5$ , where  $R^3$  and  $R^4$  are as defined above, and  $R^5$  is hydrogen,  $(C_1-C_6)$ alkyl, hydroxy-, alkoxy-, or alkylthio- substituted  $(C_1-C_6)$ alkyl, or  $R^6$  and  $R^7$  taken together complete an alicyclic or heterocyclic system;

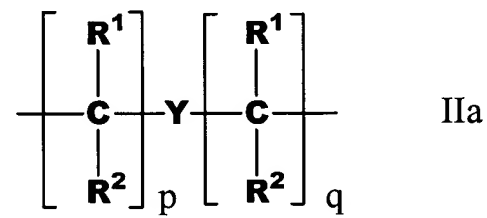
each of  $D^1$ - $D^n$  is  $(CR^6R^7)_z$  where  $R^6$  and  $R^7$  are as defined above;

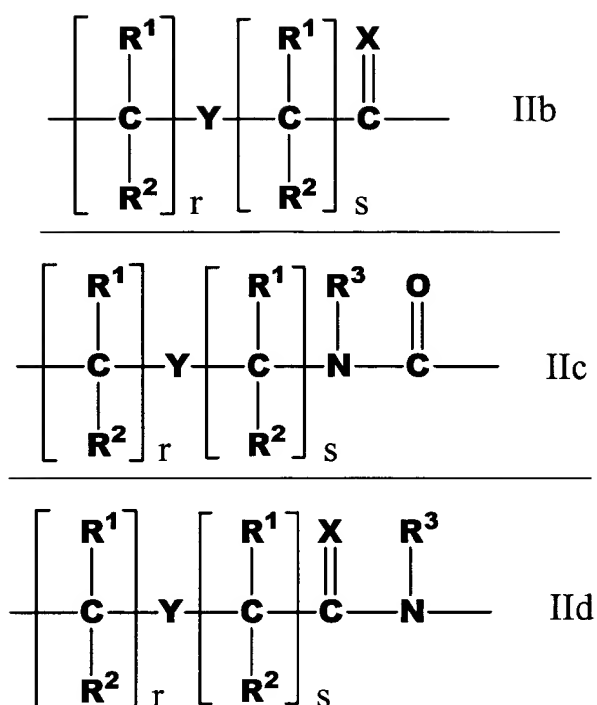
each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

each of  $G^1$ - $G^{n-1}$  is  $-NR^3CO-$ ,  $-NR^3CS-$ ,  $-NR^3SO-$  or  $-NR^3SO_2-$ , in either orientation, where  $R^3$  is as defined above;

each of  $A^1$ - $A^n$  and  $B^1$ - $B^n$  are selected such that:

- (a) A is a group of the formula (IIa), (IIb), (IIc), or (IId), and B is N or  $R^3N^+$ ; or
- (b) A is a group of formula (IId) and B is CH;





where:

X is O, S, Se, NR<sup>3</sup>, CH<sub>2</sub> or C(CH<sub>3</sub>)<sub>2</sub>;

Y is a single bond, O, S or NR<sup>4</sup>;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R<sup>1</sup> and R<sup>2</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R<sup>3</sup> and R<sup>4</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy, alkoxy, alkylthio and amino;

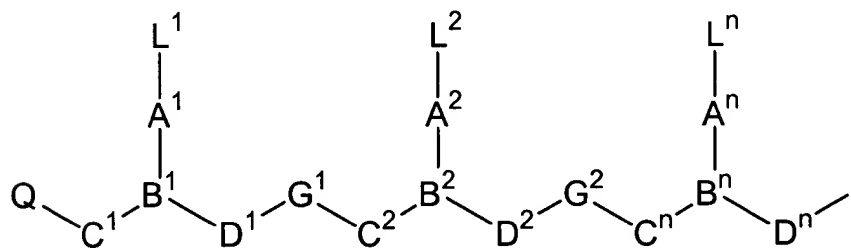
Q is -CO<sub>2</sub>H, -CONR'R'', -SO<sub>3</sub>H or -SO<sub>2</sub>NR'R'' or an activated derivative of -CO<sub>2</sub>H or -SO<sub>3</sub>H; and

I is -NHR'''R'''' or -NR'''C(O)R'''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl,

amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids;

34. (Currently Amended) A probe set comprising ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length suitable for detecting the presence, absence or number of human chromosome 12 in a sample wherein the probing nucleobase sequence of at least one probe comprises a segment, at least a portion of which is, at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

TCC-TGT-AAT-GTT-CGA-CAG (Seq. ID No. 84); TCA-TAG-AAC-GCT-AGA-AAG (Seq. ID No. 85); ACC-TTT-CTT-TTG-ATG-AAG-GA (Seq. ID No. 86); CAA-ATA-TCA-CAA-AAA-GAG-GG (Seq. ID No. 87); GAG-TTG-AAT-AGA-GGC-AAC (Seq. ID No. 88); GGC-CAA-ATG-TAG-AAA-AGG (Seq. ID No. 89); GCG-TTC-AAC-TCA-AGG-TGT (Seq. ID No. 90); TGT-CCT-TTA-GAC-AGA-GCA (Seq. ID No. 91); TGA-GAC-CAA-ATG-TAC-AAA-AG (Seq. ID No. 92); GAA-TAC-TGA-GTA-AGT-TCT-TTG (Seq. ID No. 93); AAC-TGC-ACA-AAT-AGG-GTG (Seq. ID No. 94); TGG-AGA-CAC-TGT-GTT-TGT (Seq. ID No. 95) and CCA-GTT-GGA-GAT-TTC-AAT (Seq. ID No. 96) wherein said PNA probes have the formula:



wherein,

n is at least 2,

each of L<sup>1</sup>-L<sup>n</sup> is independently selected from the group consisting of hydrogen,

hydroxy, (C<sub>1</sub>-C<sub>4</sub>)alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C<sup>1</sup>-C<sup>n</sup> is (CR<sup>6</sup>R<sup>7</sup>)<sub>y</sub> where R<sup>6</sup> is hydrogen and R<sup>7</sup> is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R<sup>6</sup> and R<sup>7</sup> are independently selected from the group consisting of hydrogen, (C<sub>2</sub>-C<sub>6</sub>)alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C<sub>1</sub>-C<sub>6</sub>)alkoxy, (C<sub>1</sub>-C<sub>6</sub>)alkylthio, NR<sup>3</sup>R<sup>4</sup> and SR<sup>5</sup>, where R<sup>3</sup> and R<sup>4</sup> are as defined above, and R<sup>5</sup> is hydrogen, (C<sub>1</sub>-C<sub>6</sub>)alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C<sub>1</sub>-C<sub>6</sub>)alkyl, or R<sup>6</sup> and R<sup>7</sup> taken together complete an alicyclic or heterocyclic system;

each of D<sup>1</sup>-D<sup>n</sup> is (CR<sup>6</sup>R<sup>7</sup>)<sub>z</sub> where R<sup>6</sup> and R<sup>7</sup> are as defined above;

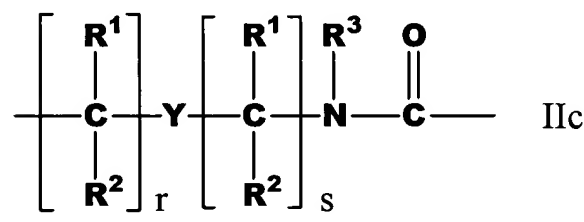
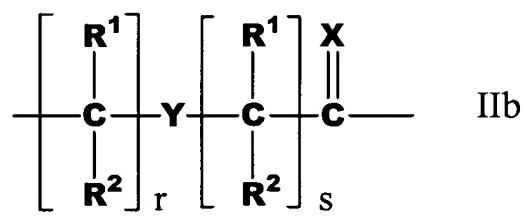
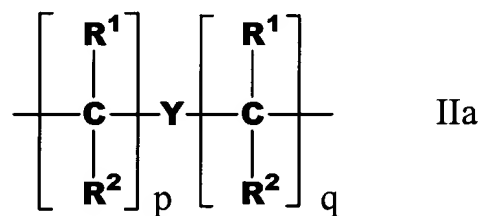
each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

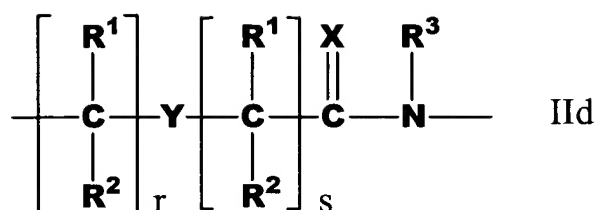
each of G<sup>1</sup>-G<sup>n-1</sup> is -NR<sup>3</sup>CO-, -NR<sup>3</sup>CS-, -NR<sup>3</sup>SO- or -NR<sup>3</sup>SO<sub>2</sub>-, in either orientation, where R<sup>3</sup> is as defined above;

each of A<sup>1</sup>-A<sup>n</sup> and B<sup>1</sup>-B<sup>n</sup> are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (IIe), and B is N or R<sup>3</sup>N<sup>+</sup>; or

(b) A is a group of formula (IIe) and B is CH;





where:

X is O, S, Se, NR<sup>3</sup>, CH<sub>2</sub> or C(CH<sub>3</sub>)<sub>2</sub>;

Y is a single bond, O, S or NR<sup>4</sup>;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R<sup>1</sup> and R<sup>2</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R<sup>3</sup> and R<sup>4</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is -CO<sub>2</sub>H, -CONR'R'', -SO<sub>3</sub>H or -SO<sub>2</sub>NR'R'' or an activated derivative of -CO<sub>2</sub>H or -SO<sub>3</sub>H; and

I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids;

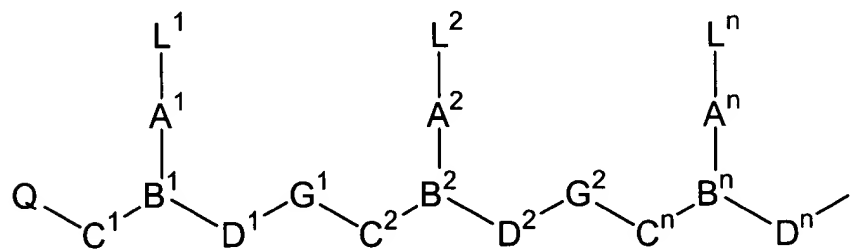
(Claims 35-37 Canceled)

38. (Currently Amended) A method for detecting, identifying or quantitating one or more of human chromosomes Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 or 18 in a sample, said method comprising:

- a) contacting the sample with one or more ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length having comprising a probing nucleobase

sequence which is specific for one or more of human chromosomes Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 or 18; and

- b) detecting, identify or quantitating hybridization of the probing nucleobase sequence of ~~non-nucleic acid~~ the PNA probe or probes to the target sequences of the chromosomes, and correlating the result with the presence, absence or number of the chromosomes in the sample wherein said PNA probe or probes have the formula:



wherein,

n is at least 2,

each of  $L^1$ - $L^n$  is independently selected from the group consisting of hydrogen, hydroxy,  $(C_1-C_4)$ alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of  $C^1$ - $C^n$  is  $(CR^6R^7)_y$ , where  $R^6$  is hydrogen and  $R^7$  is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or  $R^6$  and  $R^7$  are independently selected from the group consisting of hydrogen,  $(C_2-C_6)$ alkyl, aryl, aralkyl, heteroaryl, hydroxy,  $(C_1-C_6)$ alkoxy,  $(C_1-C_6)$ alkylthio,  $NR^3R^4$  and  $SR^5$ , where  $R^3$  and  $R^4$  are as defined above, and  $R^5$  is hydrogen,  $(C_1-C_6)$ alkyl, hydroxy-, alkoxy-, or alkylthio- substituted  $(C_1-C_6)$ alkyl, or  $R^6$  and  $R^7$  taken together complete an alicyclic or heterocyclic system;

each of  $D^1$ - $D^n$  is  $(CR^6R^7)_z$ , where  $R^6$  and  $R^7$  are as defined above;

each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

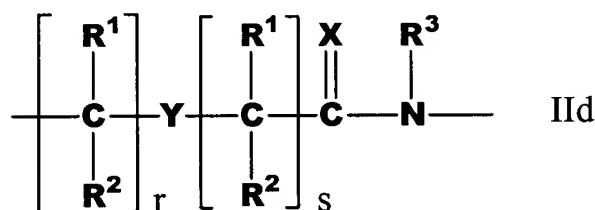
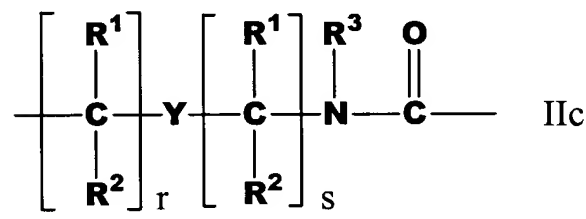
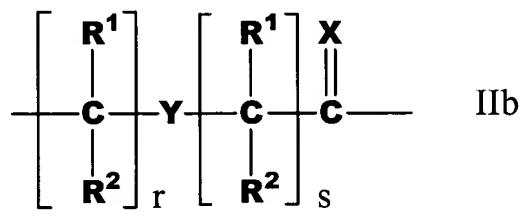
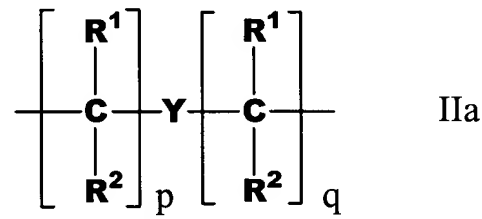
each of  $G^1$ - $G^{n-1}$  is  $-NR^3CO-$ ,  $-NR^3CS-$ ,  $-NR^3SO-$  or  $-NR^3SO_2-$ , in either orientation, where  $R^3$  is as defined above;



each of  $A^1-A^n$  and  $B^1-B^n$  are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (IIId), and B is N or  $R^3N^+$ ; or

(b) A is a group of formula (IIId) and B is  $CH_3$ ;



where:

X is O, S, Se,  $NR^3$ ,  $CH_2$  or  $C(CH_3)_2$ ;

Y is a single bond, O, S or  $NR^4$ ;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each  $R^1$  and  $R^2$  is independently selected from the group consisting of hydrogen,  $(C_1-C_4)$ alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R<sup>3</sup> and R<sup>4</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy, alkoxy, alkylthio and amino;  
Q is -CO<sub>2</sub>H, -CONR'R'', -SO<sub>3</sub>H or -SO<sub>2</sub>NR'R'' or an activated derivative of -CO<sub>2</sub>H or -SO<sub>3</sub>H; and  
I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.

39. (Original) The method of claim 38, wherein the probing nucleobase sequence of at least one probe of the set comprises a segment, at least a portion of which is, at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT (Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC (Seq. ID No. 14); CAG-AAG-AGA-TTG-AAC-CTT (Seq. ID No. 15); GGC-ATA-GCA-CAT-AAC-ATG (Seq. ID No. 16); AAT-CGT-CAT-CGA-ATG-AAT (Seq. ID No. 17); CAT-TGA-ACA-GAA-TTG-AAT (Seq. ID No. 18); GTT-TTC-AGG-GGA-AGA-TAT (Seq. ID No. 19); TGT-GCG-CCC-TCA-ACT-AAC (Seq. ID No. 20); GAA-GCT-TCA-TTG-GGA-TGT (Seq. ID No. 21); CCA-ATA-AAA-GCT-ACA-TAG-A (Seq. ID No. 22); GAA-AAA-GTT-TCT-GAC-ATT-GC (Seq. ID No. 23); TAG-TTG-AAG-GGC-ACA-TCA (Seq. ID No. 24); CAC-AAA-TAA-GAT-TCT-AAG-AAT (Seq. ID No. 25); TCA-AAA-GAA-TGC-TTC-AAC-AC (Seq. ID No. 26); ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27); GCT-GTT-TTC-TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-AAG-AGG-TCC (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-AAG (Seq. ID No. 30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No. 31); TGT-GTA-TCA-ACT-CAC-GGA (Seq. ID No. 32); CCT-CAC-AAA-GTA-GAA-ACT (Seq. ID No. 33); GAA-AAA-GCA-GTT-ACT-GAG (Seq. ID No. 34);

TAA-TAA-TTA-GAC-GGA-ATC-AT (Seq. ID No. 35); TTA-CAG-GGC-ATT-GAA-GCC (Seq. ID No. 36); CAG-TTA-TGA-AGC-AGT-CTC (Seq. ID No. 37); CAC-ACC-AGA-AAA-AGC-AGT (Seq. ID No. 38); AAG-GGT-AAA-CAC-TGT-GAG (Seq. ID No. 39); AGA-CAA-CGA-AAT-ATC-TTC-ATG (Seq. ID No. 40); CTA-GCA-GTA-TGA-GGT-CAA (Seq. ID No. 41); GCA-GAC-TTC-AGA-AAC-AGA (Seq. ID No. 42); GGC-CTC-AAA-GAC-GTT-TAA (Seq. ID No. 43); GTG-AAA-GTT-CCA-AGT-GAA (Seq. ID No. 44); GAG-TGC-TTT-GAA-GCC-TAC (Seq. ID No. 45); GAA-ACA-GCA-GAG-TTG-AAA (Seq. ID No. 46); TGC-AGA-GAT-CAC-AAC-GTG (Seq. ID No. 47); ACA-AAG-AAT-CAT-TCG-CAG (Seq. ID No. 48); AGT-GTT-AGA-AAA-CTG-CTC (Seq. ID No. 49); CTG-TTC-AGA-GTA-ACA-TGA (Seq. ID No. 50); CCG-CTT-GGA-AAT-ACT-ACA (Seq. ID No. 51); GAA-ATG-GAA-ATA-TCT-CCC-C (Seq. ID No. 52); TCT-AGG-AGG-TCC-AAT-TAT (Seq. ID No. 53); GAA-TTC-CCA-AGT-GGA-TAT (Seq. ID No. 54); CTG-TAG-GTT-TAG-ATG-AAG (Seq. ID No. 55); AAG-GAG-TGT-TTC-CCA-ACT (Seq. ID No. 56); GGC-TTC-AAG-GCG-CTC-TAA (Seq. ID No. 57); GCA-GAG-ACT-TCA-AAG-TGC (Seq. ID No. 58); CAC-ACA-CAC-GGT-GGA-CCA (Seq. ID No. 59); CAA-AGG-GAA-TGT-TCC-ATT (Seq. ID No. 60); CAC-ATA-GCA-GTG-TTT-GAG (Seq. ID No. 61); CTC-AAG-GCG-GTC-CAA-TTA (Seq. ID No. 62); GAG-TCG-AAA-TGC-ACA-CAT (Seq. ID No. 63); TAC-CAA-GAG-GAA-TGT-TGC (Seq. ID No. 64); ACG-GGA-TGC-AAT-ATA-AAA (Seq. ID No. 65); TGA-AGA-TTC-TGC-ATA-CGG (Seq. ID No. 66); AAG-GTT-TGT-ACT-GAC-AGA (Seq. ID No. 67); CTG-AAC-TAT-GGT-GAA-AAA (Seq. ID No. 68); ACT-AAC-TGT-GCT-GAA-CAT (Seq. ID No. 69); CCC-ATG-AAT-GCG-AGA-TAG (Seq. ID No. 70); AAC-TGA-ACG-CAC-AGA-TGA (Seq. ID No. 71); GGC-TAA-TCT-TTG-AAA-TTG-AAA (Seq. ID No. 72); AGG-TGG-ATA-ATT-GGC-CCT (Seq. ID No. 73); TGA-AGT-CCA-AAA-AAG-CAC (Seq. ID No. 74); CTT-AGA-CAT-GGA-AAT-ATC (Seq. ID No. 75); AAG-GGG-TCT-AAC-TAA-TCA (Seq. ID No. 76); GTA-GTT-GTT-GAG-AAT-GAT (Seq. ID No. 77); AAC-TTC-CCA-GAA-CTA-CAC (Seq. ID No. 78); ATT-CTT-GAA-ATG-GAA-CAC (Seq. ID No. 79); CTG-TGA-TTG-CTG-ATT-TGG (Seq. ID No. 80); GTC-ATC-ACA-GGA-AAC-ATT (Seq. ID No.

81); GAA-ATT-TCC-TGT-TGA-CAG-A (Seq. ID No. 82); GTT-TGA-AAG-CTG-AAC-TAT-G (Seq. ID No. 83); TCC-TGT-AAT-GTT-CGA-CAG (Seq. ID No. 84); TCA-TAG-AAC-GCT-AGA-AAG (Seq. ID No. 85); ACC-TTT-CTT-TTG-ATG-AAG-GA (Seq. ID No. 86); CAA-ATA-TCA-CAA-AAA-GAG-GG (Seq. ID No. 87); GAG-TTG-AAT-AGA-GGC-AAC (Seq. ID No. 88); GGC-CAA-ATG-TAG-AAA-AGG (Seq. ID No. 89); GCG-TTC-AAC-TCA-AGG-TGT (Seq. ID No. 90); TGT-CCT-TTA-GAC-AGA-GCA (Seq. ID No. 91); TGA-GAC-CAA-ATG-TAC-AAA-AG (Seq. ID No. 92); GAA-TAC-TGA-GTA-AGT-TCT-TTG (Seq. ID No. 93); AAC-TGC-ACA-AAT-AGG-GTG (Seq. ID No. 94); TGG-AGA-CAC-TGT-GTT-TGT (Seq. ID No. 95); CCA-GTT-GGA-GAT-TTC-AAT (Seq. ID No. 96); GAA-GCC-TGC-CAG-TGG-ATA (Seq. ID No. 97); TAC-AGC-ATT-CTG-GAA-ACC (Seq. ID No. 98); CCA-GAC-ACT-GCG-TAG-TGA (Seq. ID No. 99); ATA-TAA-TGC-TAG-AGG-GAG (Seq. ID No. 100); AAA-AAC-AAG-ACA-AAC-TCG (Seq. ID No. 101); ATT-TCA-GCT-GAC-TAA-ACA (Seq. ID No. 102); AAC-GAA-TTA-TGG-TCA-CAT (Seq. ID No. 103); GGT-GAC-GAC-TGA-GTT-TAA (Seq. ID No. 104); TTT-GGA-CCA-CTC-TGT-GGC (Seq. ID No. 105); AAC-GGG-ATA-ACT-GCA-CCT (Seq. ID No. 106); TTT-GTG-GTT-TGT-GGT-GGA (Seq. ID No. 107); AGG-GAA-TAG-CTT-CAT-AGA (Seq. ID No. 108); ATC-ACG-AAG-AAG-GTT-CTG (Seq. ID No. 109); CCG-AAG-ATG-TCT-TTG-GAA (Seq. ID No. 110); AAA-GAG-GTC-TAC-ATG-TCC (Seq. ID No. 111); TTC-CCG-TAA-CAA-CTA-TGC (Seq. ID No. 112); TCC-CGT-AAC-AAC-TAG-GCA (Seq. ID No. 113); AAA-AGG-AGT-GAT-CCA-ACC (Seq. ID No. 114); TCC-CTT-TGG-TAG-AGC-AGG (Seq. ID No. 115); ATT-TGA-GAT-GTG-TGT-ACT-CA (Seq. ID No. 116); GCA-CTT-ACC-GGC-CTA-AG (Seq. ID No. 117) and CTC-AGA-AAC-TTA-CTC-GTG (Seq. ID No. 118).

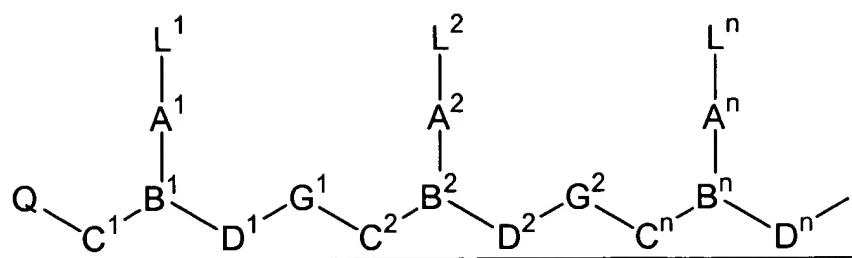
40. (Currently Amended) A method for detecting, identifying or quantitating one or more of human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 or 18 in a sample, said method comprising:

- a) contacting the sample with one or more ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length ~~having~~ comprising a probing nucleobase sequence at least a portion of which is, at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of: CTT-CAA-AGA-GGT-CCA-CGA (Seq. ID No. 1); AGG-GTT-CAA-CTG-TGT-GAC (Seq. ID No. 2); GAA-ACT-TCT-GAG-TGA-TGA (Seq. ID No. 3); CAG-TCA-TCG-CAG-AAA-ACT (Seq. ID No. 4); AGA-TTT-CAC-TGG-AAA-CGG (Seq. ID No. 5); GTT-ATG-GGA-AGG-TGA-TCC (Seq. ID No. 6); TCG-AGC-CGC-AGA-GTT-TAA (Seq. ID No. 7); CTA-TTT-AGC-GGG-CTT-GGA (Seq. ID No. 8); TAC-AAG-GGT-GTT-GCA-AAC (Seq. ID No. 9); CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT (Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC (Seq. ID No. 14); CAG-AAG-AGA-TTG-AAC-CTT (Seq. ID No. 15); GGC-ATA-GCA-CAT-AAC-ATG (Seq. ID No. 16); AAT-CGT-CAT-CGA-ATG-AAT (Seq. ID No. 17); CAT-TGA-ACA-GAA-TTG-AAT (Seq. ID No. 18); GTT-TTC-AGG-GGA-AGA-TAT (Seq. ID No. 19); TGT-GCG-CCC-TCA-ACT-AAC (Seq. ID No. 20); GAA-GCT-TCA-TTG-GGA-TGT (Seq. ID No. 21); CCA-ATA-AAA-GCT-ACA-TAG-A (Seq. ID No. 22); GAA-AAA-GTT-TCT-GAC-ATT-GC (Seq. ID No. 23); TAG-TTG-AAG-GGC-ACA-TCA (Seq. ID No. 24); CAC-AAA-TAA-GAT-TCT-AAG-AAT (Seq. ID No. 25); TCA-AAA-GAA-TGC-TTC-AAC-AC (Seq. ID No. 26); ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27); GCT-GTT-TTC-TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-AAG-AGG-TCC (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-AAG (Seq. ID No. 30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No. 31); TGT-GTA-TCA-ACT-CAC-GGA (Seq. ID No. 32); CCT-CAC-AAA-GTA-GAA-ACT (Seq. ID No. 33); GAA-AAA-GCA-GTT-ACT-GAG (Seq. ID No. 34); TAA-TAA-TTA-GAC-GGA-ATC-AT (Seq. ID No. 35); TTA-CAG-GGC-ATT-GAA-GCC (Seq. ID No. 36); CAG-TTA-TGA-AGC-AGT-CTC (Seq. ID No. 37); CAC-ACC-AGA-AAA-AGC-AGT (Seq. ID

No. 38); AAG-GGT-AAA-CAC-TGT-GAG (Seq. ID No. 39); AGA-CAA-  
 CGA-AAT-ATC-TTC-ATG (Seq. ID No. 40); CTA-GCA-GTA-TGA-GGT-  
 CAA (Seq. ID No. 41); GCA-GAC-TTC-AGA-AAC-AGA (Seq. ID No. 42);  
 GGC-CTC-AAA-GAC-GTT-TAA (Seq. ID No. 43); GTG-AAA-GTT-CCA-  
 AGT-GAA (Seq. ID No. 44); GAG-TGC-TTT-GAA-GCC-TAC (Seq. ID No.  
 45); GAA-ACA-GCA-GAG-TTG-AAA (Seq. ID No. 46); TGC-AGA-GAT-  
 CAC-AAC-GTG (Seq. ID No. 47); ACA-AAG-AAT-CAT-TCG-CAG (Seq. ID  
 No. 48); AGT-GTT-AGA-AAA-CTG-CTC (Seq. ID No. 49); CTG-TTC-AGA-  
 GTA-ACA-TGA (Seq. ID No. 50); CCG-CTT-GGA-AAT-ACT-ACA (Seq. ID  
 No. 51); GAA-ATG-GAA-ATA-TCT-CCC-C (Seq. ID No. 52); TCT-AGG-  
 AGG-TCC-AAT-TAT (Seq. ID No. 53); GAA-TTC-CCA-AGT-GGA-TAT  
 (Seq. ID No. 54); CTG-TAG-GTT-TAG-ATG-AAG (Seq. ID No. 55); AAG-  
 GAG-TGT-TTC-CCA-ACT (Seq. ID No. 56); GGC-TTC-AAG-GCG-CTC-  
 TAA (Seq. ID No. 57); GCA-GAG-ACT-TCA-AAG-TGC (Seq. ID No. 58);  
 CAC-ACA-CAC-GGT-GGA-CCA (Seq. ID No. 59); CAA-AGG-GAA-TGT-  
 TCC-ATT (Seq. ID No. 60); CAC-ATA-GCA-GTG-TTT-GAG (Seq. ID No.  
 61); CTC-AAG-GCG-GTC-CAA-TTA (Seq. ID No. 62); GAG-TCG-AAA-  
 TGC-ACA-CAT (Seq. ID No. 63); TAC-CAA-GAG-GAA-TGT-TGC (Seq. ID  
 No. 64); ACG-GGA-TGC-AAT-ATA-AAA (Seq. ID No. 65); TGA-AGA-  
 TTC-TGC-ATA-CGG (Seq. ID No. 66); AAG-GTT-TGT-ACT-GAC-AGA  
 (Seq. ID No. 67); CTG-AAC-TAT-GGT-GAA-AAA (Seq. ID No. 68); ACT-  
 AAC-TGT-GCT-GAA-CAT (Seq. ID No. 69); CCC-ATG-AAT-GCG-AGA-  
 TAG (Seq. ID No. 70); AAC-TGA-ACG-CAC-AGA-TGA (Seq. ID No. 71);  
 GGC-TAA-TCT-TTG-AAA-TTG-AAA (Seq. ID No. 72); AGG-TGG-ATA-  
 ATT-GGC-CCT (Seq. ID No. 73); TGA-AGT-CCA-AAA-AAG-CAC (Seq. ID  
 No. 74); CTT-AGA-CAT-GGA-AAT-ATC (Seq. ID No. 75); AAG-GGG-TCT-  
 AAC-TAA-TCA (Seq. ID No. 76); GTA-GTT-GTT-GAG-AAT-GAT (Seq. ID  
 No. 77); AAC-TTC-CCA-GAA-CTA-CAC (Seq. ID No. 78); ATT-CTT-GAA-  
 ATG-GAA-CAC (Seq. ID No. 79); CTG-TGA-TTG-CTG-ATT-TGG (Seq. ID  
 No. 80); GTC-ATC-ACA-GGA-AAC-ATT (Seq. ID No. 81); GAA-ATT-TCC-  
 TGT-TGA-CAG-A (Seq. ID No. 82); GTT-TGA-AAG-CTG-AAC-TAT-G

(Seq. ID No. 83); TCC-TGT-AAT-GTT-CGA-CAG (Seq. ID No. 84); TCA-TAG-AAC-GCT-AGA-AAG (Seq. ID No. 85); ACC-TTT-CTT-TTG-ATG-AAG-GA (Seq. ID No. 86); CAA-ATA-TCA-CAA-AAA-GAG-GG (Seq. ID No. 87); GAG-TTG-AAT-AGA-GGC-AAC (Seq. ID No. 88); GGC-CAA-ATG-TAG-AAA-AGG (Seq. ID No. 89); GCG-TTC-AAC-TCA-AGG-TGT (Seq. ID No. 90); TGT-CCT-TTA-GAC-AGA-GCA (Seq. ID No. 91); TGA-GAC-CAA-ATG-TAC-AAA-AG (Seq. ID No. 92); GAA-TAC-TGA-GTA-AGT-TCT-TTG (Seq. ID No. 93); AAC-TGC-ACA-AAT-AGG-GTG (Seq. ID No. 94); TGG-AGA-CAC-TGT-GTT-TGT (Seq. ID No. 95); CCA-GTT-GGA-GAT-TTC-AAT (Seq. ID No. 96); GAA-GCC-TGC-CAG-TGG-ATA (Seq. ID No. 97); TAC-AGC-ATT-CTG-GAA-ACC (Seq. ID No. 98); CCA-GAC-ACT-GCG-TAG-TGA (Seq. ID No. 99); ATA-TAA-TGC-TAG-AGG-GAG (Seq. ID No. 100); AAA-AAC-AAG-ACA-AAC-TCG (Seq. ID No. 101); ATT-TCA-GCT-GAC-TAA-ACA (Seq. ID No. 102); AAC-GAA-TTA-TGG-TCA-CAT (Seq. ID No. 103); GGT-GAC-GAC-TGA-GTT-TAA (Seq. ID No. 104); TTT-GGA-CCA-CTC-TGT-GGC (Seq. ID No. 105); AAC-GGG-ATA-ACT-GCA-CCT (Seq. ID No. 106); TTT-GTG-GTT-TGT-GGT-GGA (Seq. ID No. 107); AGG-GAA-TAG-CTT-CAT-AGA (Seq. ID No. 108); ATC-ACG-AAG-AAG-GTT-CTG (Seq. ID No. 109); CCG-AAG-ATG-TCT-TTG-GAA (Seq. ID No. 110); AAA-GAG-GTC-TAC-ATG-TCC (Seq. ID No. 111); TTC-CCG-TAA-CAA-CTA-TGC (Seq. ID No. 112); TCC-CGT-AAC-AAC-TAG-GCA (Seq. ID No. 113); AAA-AGG-AGT-GAT-CCA-ACC (Seq. ID No. 114); TCC-CTT-TGG-TAG-AGC-AGG (Seq. ID No. 115); ATT-TGA-GAT-GTG-TGT-ACT-CA (Seq. ID No. 116) ; GCA-CTT-ACC-GGC-CTA-AG (Seq. ID No. 117) and CTC-AGA-AAC-TTA-CTC-GTG (Seq. ID No. 118); and

- b) detecting, identify or quantitating hybridization of the probing nucleobase sequence of ~~non-nucleic acid~~ the PNA probe or probes to the target sequences of the chromosomes, and correlating the result with the presence, absence or number of the chromosomes in the sample wherein said PNA probe or probes have the formula:



wherein,

n is at least 2,

each of  $L^1$ - $L^n$  is independently selected from the group consisting of hydrogen, hydroxy,  $(C_1-C_4)$ alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of  $C^1$ - $C^n$  is  $(CR^6R^7)_y$  where  $R^6$  is hydrogen and  $R^7$  is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or  $R^6$  and  $R^7$  are independently selected from the group consisting of hydrogen,  $(C_2-C_6)$ alkyl, aryl, aralkyl, heteroaryl, hydroxy,  $(C_1-C_6)$ alkoxy,  $(C_1-C_6)$ alkylthio,  $NR^3R^4$  and  $SR^5$ , where  $R^3$  and  $R^4$  are as defined above, and  $R^5$  is hydrogen,  $(C_1-C_6)$ alkyl, hydroxy-, alkoxy-, or alkylthio- substituted  $(C_1-C_6)$ alkyl, or  $R^6$  and  $R^7$  taken together complete an alicyclic or heterocyclic system;

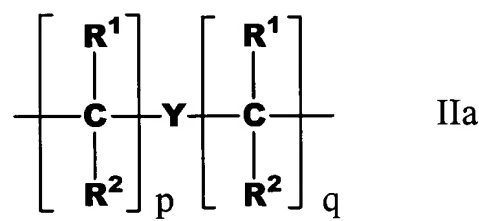
each of  $D^1$ - $D^n$  is  $(CR^6R^7)_z$  where  $R^6$  and  $R^7$  are as defined above;

each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

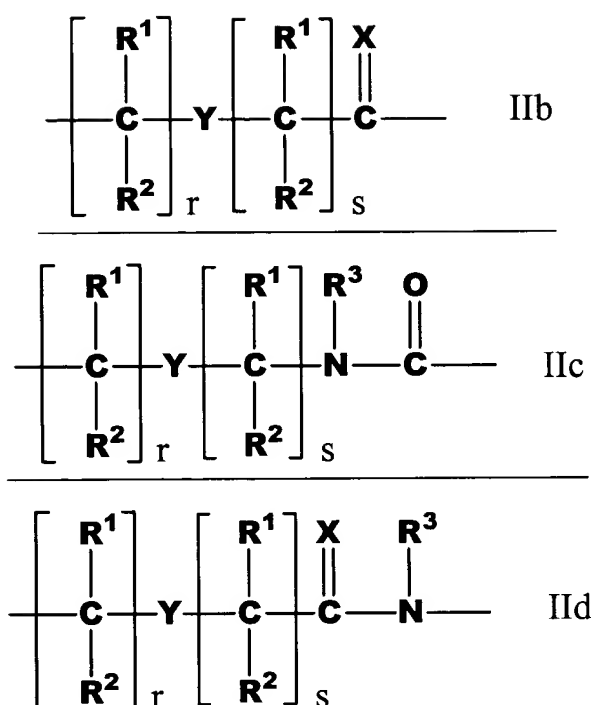
each of  $G^1$ - $G^{n-1}$  is  $-NR^3CO-$ ,  $-NR^3CS-$ ,  $-NR^3SO-$  or  $-NR^3SO_2-$ , in either orientation, where  $R^3$  is as defined above;

each of  $A^1$ - $A^n$  and  $B^1$ - $B^n$  are selected such that:

- (a) A is a group of the formula (IIa), (IIb), (IIc), or (IId), and B is N or  $R^3N^+$ ; or
- (b) A is a group of formula (IId) and B is  $CH_3$ ;







where:

X is O, S, Se, NR<sup>3</sup>, CH<sub>2</sub> or C(CH<sub>3</sub>)<sub>2</sub>;

Y is a single bond, O, S or NR<sup>4</sup>;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R<sup>1</sup> and R<sup>2</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R<sup>3</sup> and R<sup>4</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is -CO<sub>2</sub>H, -CONR'R'', -SO<sub>3</sub>H or -SO<sub>2</sub>NR'R'' or an activated derivative of -CO<sub>2</sub>H or -SO<sub>3</sub>H; and

I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl,

amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.

(Claims 41-44 canceled)

45. (Currently Amended) The method of claim 40, wherein the presence, absence or number of human chromosome 3 is determined by:

- a) contacting the sample with one or more ~~non-nucleic acid~~ PNA probes, wherein at least one probe ~~has~~ comprises a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27); GCT-GTT-TTC-TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-AAG-AGG-TCC (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-AAG (Seq. ID No. 30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No. 31); TGT-GTA-TCA-ACT-CAC-GGA (Seq. ID No. 32); CCT-CAC-AAA-GTA-GAA-ACT (Seq. ID No. 33); GAA-AAA-GCA-GTT-ACT-GAG (Seq. ID No. 34); TAA-TAA-TTA-GAC-GGA-ATC-AT (Seq. ID No. 35); TTA-CAG-GGC-ATT-GAA-GCC (Seq. ID No. 36); CAG-TTA-TGA-AGC-AGT-CTC (Seq. ID No. 37); CAC-ACC-AGA-AAA-AGC-AGT (Seq. ID No. 38); AAG-GGT-AAA-CAC-TGT-GAG (Seq. ID No. 39); AGA-CAA-CGA-AAT-ATC-TTC-ATG (Seq. ID No. 40); CTA-GCA-GTA-TGA-GGT-CAA (Seq. ID No. 41); GCA-GAC-TTC-AGA-AAC-AGA (Seq. ID No. 42); GGC-CTC-AAA-GAC-GTT-TAA (Seq. ID No. 43); GTG-AAA-GTT-CCA-AGT-GAA (Seq. ID No. 44); GAG-TGC-TTT-GAA-GCC-TAC (Seq. ID No. 45); GAA-ACA-GCA-GAG-TTG-AAA (Seq. ID No. 46); TGC-AGA-GAT-CAC-AAC-GTG (Seq. ID No. 47); ACA-AAG-AAT-CAT-TCG-CAG (Seq. ID No. 48); and AGT-GTT-AGA-AAA-CTG-CTC (Seq. ID No. 49); and

- b) detecting, identifying or quantitating hybridization of the probing nucleobase sequence of the probe or probes to a target sequence in the

sample to thereby correlate the result with the presence, absence or number of human chromosome 3 in the sample.

(Claim 46 canceled)

47. (Currently Amended) The method of claim 40, wherein the presence, absence or number of human chromosome 8 is determined by:

- a) contacting the sample with one or more ~~non-nucleic acid~~ PNA probes, wherein at least one probe ~~has~~ comprises a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

ACG-GGA-TGC-AAT-ATA-AAA (Seq. ID No. 65); TGA-AGA-TTC-TGC-ATA-CGG (Seq. ID No. 66); AAG-GTT-TGT-ACT-GAC-AGA (Seq. ID No. 67); CTG-AAC-TAT-GGT-GAA-AAA (Seq. ID No. 68); ACT-AAC-TGT-GCT-GAA-CAT (Seq. ID No. 69) and CCC-ATG-AAT-GCG-AGA-TAG (Seq. ID No. 70); and

- b) detecting, identifying or quantitating hybridization of the probing nucleobase sequence of the probe or probes to a target sequence in the sample to thereby correlate the result with the presence, absence or number of human chromosome 8 in the sample.

(Claim 48 canceled)

49. (Currently Amended) The method of claim 40, wherein the presence, absence or number of human chromosome 11 is determined by:

- a) contacting the sample with one or more ~~non-nucleic acid~~ PNA probes, wherein at least one probe ~~has~~ comprises a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

AAC-TTC-CCA-GAA-CTA-CAC (Seq. ID No. 78); ATT-CTT-GAA-ATG-GAA-CAC (Seq. ID No. 79); CTG-TGA-TTG-CTG-ATT-TGG (Seq. ID No. 80); GTC-ATC-ACA-GGA-AAC-ATT (Seq. ID No. 81); GAA-ATT-TCC-TGT-TGA-CAG-A (Seq. ID No. 82) and GTT-TGA-AAG-CTG-AAC-TAT-G (Seq. ID No. 83); and

- b) detecting, identifying or quantitating hybridization of the probing nucleobase sequence of the probe or probes to a target sequence in the sample to thereby correlate the result with the presence, absence or number of human chromosome 11 in the sample.

50. (Currently Amended) The method of claim 40, wherein the presence, absence or number of human chromosome 12 is determined by:

- a) contacting the sample with one or more ~~non-nucleic acid~~ PNA probes, wherein at least one probe ~~has~~ comprises a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

TCC-TGT-AAT-GTT-CTA-CAG (Seq. ID No. 84); TCA-TAG-AAC-GCT-AGA-AAG (Seq. ID No. 85); ACC-TTT-CTT-TTG-ATG-AAG-GA (Seq. ID No. 86); CAA-ATA-TCA-CAA-AAA-GAG-GG (Seq. ID No. 87); GAG-TTG-AAT-AGA-GGC-AAC (Seq. ID No. 88); GGC-CAA-ATG-TAG-AAA-AGG (Seq. ID No. 89); GCG-TTC-AAC-TCA-AGG-TGT (Seq. ID No. 90); TGT-CCT-TTA-GAC-AGA-GCA (Seq. ID No. 91); TGA-GAC-CAA-ATG-TAC-AAA-AG (Seq. ID No. 92); GAA-TAC-TGA-GTA-AGT-TCT-TTG (Seq. ID No. 93); AAC-TGC-ACA-AAT-AGG-GTG (Seq. ID No. 94); TGG-AGA-CAC-TGT-GTT-TGT (Seq. ID No. 95) and CCA-GTT-GGA-GAT-TTC-AAT (Seq. ID No. 96); and

- b) detecting, identifying or quantitating hybridization of the probing nucleobase sequence of the probe or probes to a target sequence in the sample to thereby correlate the result with the presence, absence or number of human chromosome 12 in the sample.

(Claims 51-53 canceled)

54. (Original) The method of claim 40, wherein the two or more probes are unlabeled.
55. (Original) The method of claim 40, wherein at least one probe is labeled with a detectable moiety.
56. (Original) The method of claim 55, wherein the detectable moiety or moieties are selected from the group consisting of: a dextran conjugate, a branched nucleic acid detection system, a chromophore, a fluorophore, a spin label, a radioisotope, an enzyme, a hapten, an acridinium ester and a chemiluminescent compound.

(Claims 57-63 canceled)

64. (Currently Amended) A kit suitable for performing an assay which detects the presence, absence or number of human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 or 18 in a sample, wherein said kit comprises:
  - a) one or more ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length wherein at least one probe ~~has~~ comprises a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:
 

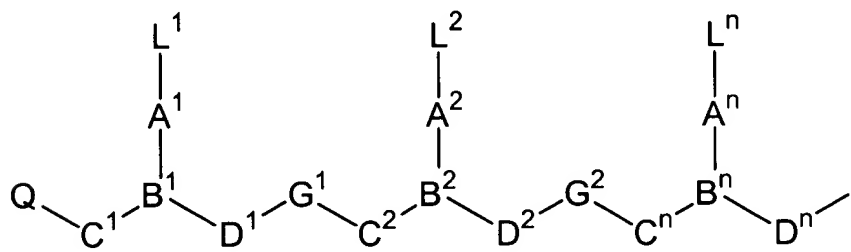
CTT-CAA-AGA-GGT-CCA-CGA (Seq. ID No. 1); AGG-GTT-CAA-CTG-TGT-GAC (Seq. ID No. 2); GAA-ACT-TCT-GAG-TGA-TGA (Seq. ID No. 3); CAG-TCA-TCG-CAG-AAA-ACT (Seq. ID No. 4); AGA-TTT-CAC-TGG-AAA-CGG (Seq. ID No. 5); GTT-ATG-GGA-AGG-TGA-TCC (Seq. ID No. 6); TCG-AGC-CGC-AGA-GTT-TAA (Seq. ID No. 7); CTA-TTT-AGC-GGG-CTT-GGA (Seq. ID No. 8); TAC-AAG-GGT-GTT-GCA-AAC (Seq. ID No. 9); CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-

AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-  
 TGA-TAT-GT (Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC  
 (Seq. ID No. 14); CAG-AAG-AGA-TTG-AAC-CTT (Seq. ID No. 15);  
 GGC-ATA-GCA-CAT-AAC-ATG (Seq. ID No. 16); AAT-CGT-CAT-  
 CGA-ATG-AAT (Seq. ID No. 17); CAT-TGA-ACA-GAA-TTG-AAT (Seq.  
 ID No. 18); GTT-TTC-AGG-GGA-AGA-TAT (Seq. ID No. 19); TGT-GCG-  
 CCC-TCA-ACT-AAC (Seq. ID No. 20); GAA-GCT-TCA-TTG-GGA-TGT  
 (Seq. ID No. 21); CCA-ATA-AAA-GCT-ACA-TAG-A (Seq. ID No. 22);  
 GAA-AAA-GTT-TCT-GAC-ATT-GC (Seq. ID No. 23); TAG-TTG-AAG-  
 GGC-ACA-TCA (Seq. ID No. 24); CAC-AAA-TAA-GAT-TCT-AAG-  
 AAT (Seq. ID No. 25); TCA-AAA-GAA-TGC-TTC-AAC-AC (Seq. ID No.  
 26); ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27); GCT-GTT-  
 TTC-TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-AAG-AGG-  
 TCC (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-AAG (Seq. ID  
 No. 30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No. 31); TGT-GTA-  
 TCA-ACT-CAC-GGA (Seq. ID No. 32); CCT-CAC-AAA-GTA-GAA-  
 ACT (Seq. ID No. 33); GAA-AAA-GCA-GTT-ACT-GAG (Seq. ID No.  
 34); TAA-TAA-TTA-GAC-GGA-ATC-AT (Seq. ID No. 35); TTA-CAG-  
 GGC-ATT-GAA-GCC (Seq. ID No. 36); CAG-TTA-TGA-AGC-AGT-CTC  
 (Seq. ID No. 37); CAC-ACC-AGA-AAA-AGC-AGT (Seq. ID No. 38);  
 AAG-GGT-AAA-CAC-TGT-GAG (Seq. ID No. 39); AGA-CAA-CGA-  
 AAT-ATC-TTC-ATG (Seq. ID No. 40); CTA-GCA-GTA-TGA-GGT-CAA  
 (Seq. ID No. 41); GCA-GAC-TTC-AGA-AAC-AGA (Seq. ID No. 42);  
 GGC-CTC-AAA-GAC-GTT-TAA (Seq. ID No. 43); GTG-AAA-GTT-  
 CCA-AGT-GAA (Seq. ID No. 44); GAG-TGC-TTT-GAA-GCC-TAC (Seq.  
 ID No. 45); GAA-ACA-GCA-GAG-TTG-AAA (Seq. ID No. 46); TGC-  
 AGA-GAT-CAC-AAC-GTG (Seq. ID No. 47); ACA-AAG-AAT-CAT-  
 TCG-CAG (Seq. ID No. 48); AGT-GTT-AGA-AAA-CTG-CTC (Seq. ID  
 No. 49); CTG-TTC-AGA-GTA-ACA-TGA (Seq. ID No. 50); CCG-CTT-  
 GGA-AAT-ACT-ACA (Seq. ID No. 51); GAA-ATG-GAA-ATA-TCT-  
 CCC-C (Seq. ID No. 52); TCT-AGG-AGG-TCC-AAT-TAT (Seq. ID No.

53); GAA-TTC-CCA-AGT-GGA-TAT (Seq. ID No. 54); CTG-TAG-GTT-TAG-ATG-AAG (Seq. ID No. 55); AAG-GAG-TGT-TTC-CCA-ACT (Seq. ID No. 56); GGC-TTC-AAG-GCG-CTC-TAA (Seq. ID No. 57); GCA-GAG-ACT-TCA-AAG-TGC (Seq. ID No. 58); CAC-ACA-CAC-GGT-GGA-CCA (Seq. ID No. 59); CAA-AGG-GAA-TGT-TCC-ATT (Seq. ID No. 60); CAC-ATA-GCA-GTG-TTT-GAG (Seq. ID No. 61); CTC-AAG-GCG-GTC-CAA-TTA (Seq. ID No. 62); GAG-TCG-AAA-TGC-ACA-CAT (Seq. ID No. 63); TAC-CAA-GAG-GAA-TGT-TGC (Seq. ID No. 64); ACG-GGA-TGC-AAT-ATA-AAA (Seq. ID No. 65); TGA-AGA-TTC-TGC-ATA-CGG (Seq. ID No. 66); AAG-GTT-TGT-ACT-GAC-AGA (Seq. ID No. 67); CTG-AAC-TAT-GGT-GAA-AAA (Seq. ID No. 68); ACT-AAC-TGT-GCT-GAA-CAT (Seq. ID No. 69); CCC-ATG-AAT-GCG-AGA-TAG (Seq. ID No. 70); AAC-TGA-ACG-CAC-AGA-TGA (Seq. ID No. 71); GGC-TAA-TCT-TTG-AAA-TTG-AAA (Seq. ID No. 72); AGG-TGG-ATA-ATT-GGC-CCT (Seq. ID No. 73); TGA-AGT-CCA-AAA-AAG-CAC (Seq. ID No. 74); CTT-AGA-CAT-GGA-AAT-ATC (Seq. ID No. 75); AAG-GGG-TCT-AAC-TAA-TCA (Seq. ID No. 76); GTA-GTT-GTT-GAG-AAT-GAT (Seq. ID No. 77); AAC-TTC-CCA-GAA-CTA-CAC (Seq. ID No. 78); ATT-CTT-GAA-ATG-GAA-CAC (Seq. ID No. 79); CTG-TGA-TTG-CTG-ATT-TGG (Seq. ID No. 80); GTC-ATC-ACA-GGA-AAC-ATT (Seq. ID No. 81); GAA-ATT-TCC-TGT-TGA-CAG-A (Seq. ID No. 82); GTT-TGA-AAG-CTG-AAC-TAT-G (Seq. ID No. 83); TCC-TGT-AAT-GTT-CGA-CAG (Seq. ID No. 84); TCA-TAG-AAC-GCT-AGA-AAG (Seq. ID No. 85); ACC-TTT-CTT-TTG-ATG-AAG-GA (Seq. ID No. 86); CAA-ATA-TCA-CAA-AAA-GAG-GG (Seq. ID No. 87); GAG-TTG-AAT-AGA-GGC-AAC (Seq. ID No. 88); GGC-CAA-ATG-TAG-AAA-AGG (Seq. ID No. 89); GCG-TTC-AAC-TCA-AGG-TGT (Seq. ID No. 90); TGT-CCT-TTA-GAC-AGA-GCA (Seq. ID No. 91); TGA-GAC-CAA-ATG-TAC-AAA-AG (Seq. ID No. 92); GAA-TAC-TGA-GTA-AGT-TCT-TTG (Seq. ID No. 93); AAC-TGC-ACA-AAT-AGG-GTG (Seq. ID No. 94); TGG-AGA-CAC-TGT-GTT-TGT (Seq. ID No. 95); CCA-GTT-GGA-GAT-

TTC-AAT (Seq. ID No. 96); GAA-GCC-TGC-CAG-TGG-ATA (Seq. ID No. 97); TAC-AGC-ATT-CTG-GAA-ACC (Seq. ID No. 98); CCA-GAC-ACT-GCG-TAG-TGA (Seq. ID No. 99); ATA-TAA-TGC-TAG-AGG-GAG (Seq. ID No. 100); AAA-AAC-AAG-ACA-AAC-TCG (Seq. ID No. 101); ATT-TCA-GCT-GAC-TAA-ACA (Seq. ID No. 102); AAC-GAA-TTA-TGG-TCA-CAT (Seq. ID No. 103); GGT-GAC-GAC-TGA-GTT-TAA (Seq. ID No. 104); TTT-GGA-CCA-CTC-TGT-GGC (Seq. ID No. 105); AAC-GGG-ATA-ACT-GCA-CCT (Seq. ID No. 106); TTT-GTG-GTT-TGT-GGT-GGA (Seq. ID No. 107); AGG-GAA-TAG-CTT-CAT-AGA (Seq. ID No. 108); ATC-ACG-AAG-AAG-GTT-CTG (Seq. ID No. 109); CCG-AAG-ATG-TCT-TTG-GAA (Seq. ID No. 110); AAA-GAG-GTC-TAC-ATG-TCC (Seq. ID No. 111); TTC-CCG-TAA-CAA-CTA-TGC (Seq. ID No. 112); TCC-CGT-AAC-AAC-TAG-GCA (Seq. ID No. 113); AAA-AGG-AGT-GAT-CCA-ACC (Seq. ID No. 114); TCC-CTT-TGG-TAG-AGC-AGG (Seq. ID No. 115); ATT-TGA-GAT-GTG-TGT-ACT-CA (Seq. ID No. 116); GCA-CTT-ACC-GGC-CTA-AG (Seq. ID No. 117) and CTC-AGA-AAC-TTA-CTC-GTG (Seq. ID No. 118); and

- b) other reagents or compositions necessary to perform the assay wherein said PNA probe or probes have the formula:



wherein,

n is at least 2,

each of L<sup>1</sup>-L<sup>n</sup> is independently selected from the group consisting of hydrogen, hydroxy, (C<sub>1</sub>-C<sub>4</sub>)alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;



each of C<sup>1</sup>-C<sup>n</sup> is (CR<sup>6</sup>R<sup>7</sup>)<sub>y</sub> where R<sup>6</sup> is hydrogen and R<sup>7</sup> is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R<sup>6</sup> and R<sup>7</sup> are independently selected from the group consisting of hydrogen, (C<sub>2</sub>-C<sub>6</sub>)alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C<sub>1</sub>-C<sub>6</sub>)alkoxy, (C<sub>1</sub>-C<sub>6</sub>)alkylthio, NR<sup>3</sup>R<sup>4</sup> and SR<sup>5</sup>, where R<sup>3</sup> and R<sup>4</sup> are as defined above, and R<sup>5</sup> is hydrogen, (C<sub>1</sub>-C<sub>6</sub>)alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C<sub>1</sub>-C<sub>6</sub>)alkyl, or R<sup>6</sup> and R<sup>7</sup> taken together complete an alicyclic or heterocyclic system;

each of D<sup>1</sup>-D<sup>n</sup> is (CR<sup>6</sup>R<sup>7</sup>)<sub>z</sub> where R<sup>6</sup> and R<sup>7</sup> are as defined above;

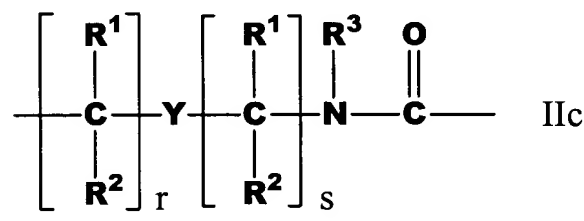
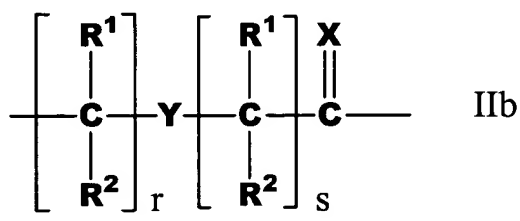
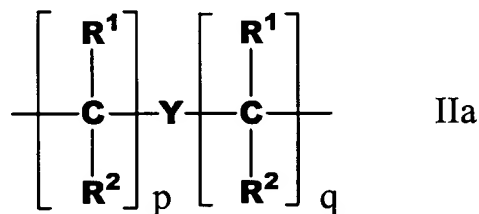
each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

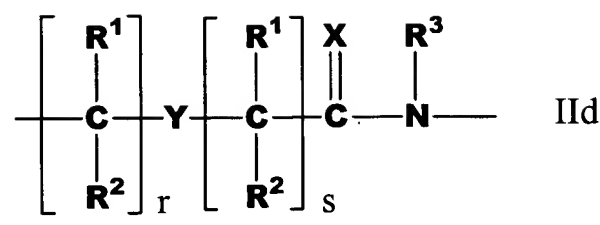
each of G<sup>1</sup>-G<sup>n-1</sup> is -NR<sup>3</sup>CO-, -NR<sup>3</sup>CS-, -NR<sup>3</sup>SO- or -NR<sup>3</sup>SO<sub>2</sub>-, in either orientation, where R<sup>3</sup> is as defined above;

each of A<sup>1</sup>-A<sup>n</sup> and B<sup>1</sup>-B<sup>n</sup> are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (IIe), and B is N or R<sup>3</sup>N<sup>+</sup>; or

(b) A is a group of formula (IIe) and B is CH;





where:

X is O, S, Se, NR<sup>3</sup>, CH<sub>2</sub> or C(CH<sub>3</sub>)<sub>2</sub>;

Y is a single bond, O, S or NR<sup>4</sup>;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R<sup>1</sup> and R<sup>2</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R<sup>3</sup> and R<sup>4</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy, alkoxy, alkylthio and amino;

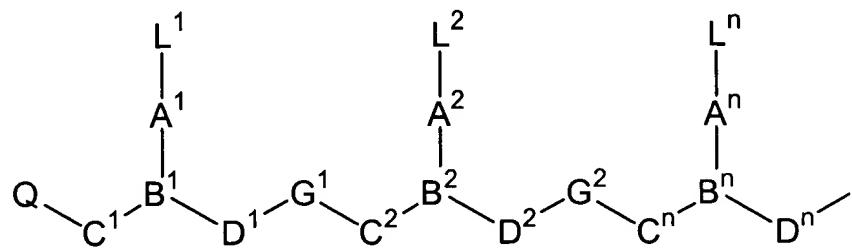
Q is -CO<sub>2</sub>H, -CONR'R'', -SO<sub>3</sub>H or -SO<sub>2</sub>NR'R'' or an activated derivative of -CO<sub>2</sub>H or -SO<sub>3</sub>H; and

I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.

65. (Original) The kit of claim 64, wherein at the probe or probes are unlabeled.
66. (Original) The kit of claim 65, wherein hybridization of the probing nucleobase sequence of the probe to the chromosome is detected using an antibody or antibody fragment, wherein the antibody or antibody fragment specifically binds, under antibody binding conditions, to the PNA/nucleic acid complex which forms under suitable hybridization conditions.

(Claims 67-77 canceled)

78. (Currently Amended) A multiplex assay using ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length to detect, identify or enumerate two or more human chromosomes in the sample wherein said PNA probes have the formula:



wherein,

n is at least 2,

each of  $L^1$ - $L^n$  is independently selected from the group consisting of hydrogen, hydroxy,  $(C_1-C_4)$ alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of  $C^1$ - $C^n$  is  $(CR^6R^7)_x$  where  $R^6$  is hydrogen and  $R^7$  is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or  $R^6$  and  $R^7$  are independently selected from the group consisting of hydrogen,  $(C_2-C_6)$ alkyl, aryl, aralkyl, heteroaryl, hydroxy,  $(C_1-C_6)$ alkoxy,  $(C_1-C_6)$ alkylthio,  $NR^3R^4$  and  $SR^5$ , where  $R^3$  and  $R^4$  are as defined above, and  $R^5$  is hydrogen,  $(C_1-C_6)$ alkyl, hydroxy-, alkoxy-, or alkylthio- substituted  $(C_1-C_6)$ alkyl, or  $R^6$  and  $R^7$  taken together complete an alicyclic or heterocyclic system;

each of  $D^1$ - $D^n$  is  $(CR^6R^7)_z$  where  $R^6$  and  $R^7$  are as defined above;

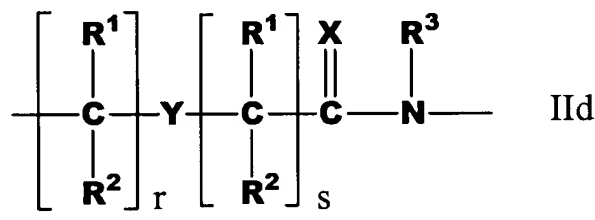
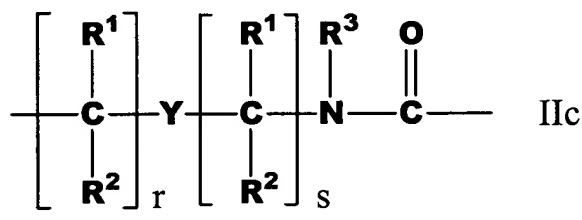
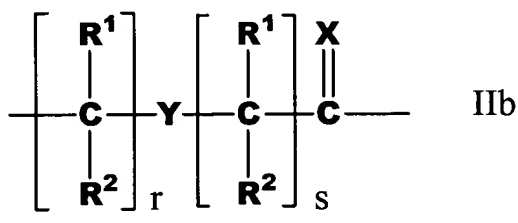
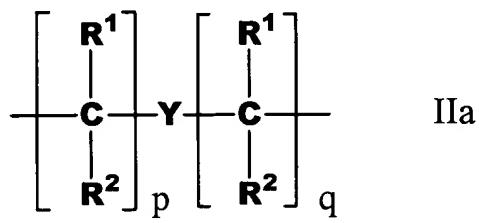
each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

each of  $G^1$ - $G^{n-1}$  is  $-NR^3CO-$ ,  $-NR^3CS-$ ,  $-NR^3SO-$  or  $-NR^3SO_2-$ , in either orientation, where  $R^3$  is as defined above;

each of  $A^1$ - $A^n$  and  $B^1$ - $B^n$  are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (IIId), and B is N or R<sup>3</sup>N<sup>+</sup>; or

(b) A is a group of formula (IIId) and B is CH;



where:

X is O, S, Se, NR<sup>3</sup>, CH<sub>2</sub> or C(CH<sub>3</sub>)<sub>2</sub>;

Y is a single bond, O, S or NR<sup>4</sup>;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R<sup>1</sup> and R<sup>2</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R<sup>3</sup> and R<sup>4</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy, alkoxy, alkylthio and amino;  
Q is -CO<sub>2</sub>H, -CONR'R'', -SO<sub>3</sub>H or -SO<sub>2</sub>NR'R'' or an activated derivative of -CO<sub>2</sub>H or -SO<sub>3</sub>H; and  
I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.

79. (Original) The multiplex assay of claim 78, wherein the assay is used to detect, identify or enumerate two or more human chromosomes selected from the group consisting of: X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and 18.
80. (Currently Amended) The multiplex assay of claim 78, wherein at least two ~~non-nucleic acid~~ PNA probes are independently detectable such that each of the two or more probes can detect the presence, absence or number of one of human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 or 18.
81. (Currently Amended) The multiplex assay of claim 80, wherein one or more of the ~~non-nucleic acid~~ PNA probes comprise a probing nucleobase sequence, at least a portion of which is, at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of: CTT-CAA-AGA-GGT-CCA-CGA (Seq. ID No. 1); AGG-GTT-CAA-CTG-TGT-GAC (Seq. ID No. 2); GAA-ACT-TCT-GAG-TGA-TGA (Seq. ID No. 3); CAG-TCA-TCG-CAG-AAA-ACT (Seq. ID No. 4); AGA-TTT-CAC-TGG-AAA-CGG (Seq. ID No. 5); GTT-ATG-GGA-AGG-TGA-TCC (Seq. ID No. 6); TCG-AGC-CGC-AGA-GTT-TAA (Seq. ID No. 7); CTA-TTT-AGC-GGG-CTT-GGA (Seq. ID No. 8); TAC-AAG-GGT-GTT-GCA-AAC (Seq. ID No. 9); CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT

(Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC (Seq. ID No. 14); CAG-AAG-AGA-TTG-AAC-CTT (Seq. ID No. 15); GGC-ATA-GCA-CAT-AAC-ATG (Seq. ID No. 16); AAT-CGT-CAT-CGA-ATG-AAT (Seq. ID No. 17); CAT-TGA-ACA-GAA-TTG-AAT (Seq. ID No. 18); GTT-TTC-AGG-GGA-AGA-TAT (Seq. ID No. 19); TGT-GCG-CCC-TCA-ACT-AAC (Seq. ID No. 20); GAA-GCT-TCA-TTG-GGA-TGT (Seq. ID No. 21); CCA-ATA-AAA-GCT-ACA-TAG-A (Seq. ID No. 22); GAA-AAA-GTT-TCT-GAC-ATT-GC (Seq. ID No. 23); TAG-TTG-AAG-GGC-ACA-TCA (Seq. ID No. 24); CAC-AAA-TAA-GAT-TCT-AAG-AAT (Seq. ID No. 25); TCA-AAA-GAA-TGC-TTC-AAC-AC (Seq. ID No. 26); ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27); GCT-GTT-TTC-TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-AAG-AGG-TCC (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-AAG (Seq. ID No. 30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No. 31); TGT-GTA-TCA-ACT-CAC-GGA (Seq. ID No. 32); CCT-CAC-AAA-GTA-GAA-ACT (Seq. ID No. 33); GAA-AAA-GCA-GTT-ACT-GAG (Seq. ID No. 34); TAA-TAA-TTA-GAC-GGA-ATC-AT (Seq. ID No. 35); TTA-CAG-GGC-ATT-GAA-GCC (Seq. ID No. 36); CAG-TTA-TGA-AGC-AGT-CTC (Seq. ID No. 37); CAC-ACC-AGA-AAA-AGC-AGT (Seq. ID No. 38); AAG-GGT-AAA-CAC-TGT-GAG (Seq. ID No. 39); AGA-CAA-CGA-AAT-ATC-TTC-ATG (Seq. ID No. 40); CTA-GCA-GTA-TGA-GGT-CAA (Seq. ID No. 41); GCA-GAC-TTC-AGA-AAC-AGA (Seq. ID No. 42); GGC-CTC-AAA-GAC-GTT-TAA (Seq. ID No. 43); GTG-AAA-GTT-CCA-AGT-GAA (Seq. ID No. 44); GAG-TGC-TTT-GAA-GCC-TAC (Seq. ID No. 45); GAA-ACA-GCA-GAG-TTG-AAA (Seq. ID No. 46); TGC-AGA-GAT-CAC-AAC-GTG (Seq. ID No. 47); ACA-AAG-AAT-CAT-TCG-CAG (Seq. ID No. 48); AGT-GTT-AGA-AAA-CTG-CTC (Seq. ID No. 49); CTG-TTC-AGA-GTA-ACA-TGA (Seq. ID No. 50); CCG-CTT-GGA-AAT-ACT-ACA (Seq. ID No. 51); GAA-ATG-GAA-ATA-TCT-CCC-C (Seq. ID No. 52); TCT-AGG-AGG-TCC-AAT-TAT (Seq. ID No. 53); GAA-TTC-CCA-AGT-GGA-TAT (Seq. ID No. 54); CTG-TAG-GTT-TAG-ATG-AAG (Seq. ID No. 55); AAG-GAG-TGT-TTC-CCA-ACT (Seq. ID No. 56); GGC-TTC-AAG-GCG-CTC-TAA (Seq. ID No. 57); GCA-GAG-ACT-TCA-AAG-TGC (Seq. ID No. 58); CAC-ACA-CAC-GGT-GGA-CCA (Seq. ID No. 59); CAA-AGG-GAA-TGT-TCC-ATT (Seq. ID No. 60); CAC-ATA-GCA-GTG-TTT-GAG (Seq. ID No. 61); CTC-AAG-GCG-GTC-CAA-TTA

(Seq. ID No. 62); GAG-TCG-AAA-TGC-ACA-CAT (Seq. ID No. 63); TAC-CAA-GAG-GAA-TGT-TGC (Seq. ID No. 64); ACG-GGA-TGC-AAT-ATA-AAA (Seq. ID No. 65); TGA-AGA-TTC-TGC-ATA-CGG (Seq. ID No. 66); AAG-GTT-TGT-ACT-GAC-AGA (Seq. ID No. 67); CTG-AAC-TAT-GGT-GAA-AAA (Seq. ID No. 68); ACT-AAC-TGT-GCT-GAA-CAT (Seq. ID No. 69); CCC-ATG-AAT-GCG-AGA-TAG (Seq. ID No. 70); AAC-TGA-ACG-CAC-AGA-TGA (Seq. ID No. 71); GGC-TAA-TCT-TTG-AAA-TTG-AAA (Seq. ID No. 72); AGG-TGG-ATA-ATT-GGC-CCT (Seq. ID No. 73); TGA-AGT-CCA-AAA-AAG-CAC (Seq. ID No. 74); CTT-AGA-CAT-GGA-AAT-ATC (Seq. ID No. 75); AAG-GGG-TCT-AAC-TAA-TCA (Seq. ID No. 76); GTA-GTT-GTT-GAG-AAT-GAT (Seq. ID No. 77); AAC-TTC-CCA-GAA-CTA-CAC (Seq. ID No. 78); ATT-CTT-GAA-ATG-GAA-CAC (Seq. ID No. 79); CTG-TGA-TTG-CTG-ATT-TGG (Seq. ID No. 80); GTC-ATC-ACA-GGA-AAC-ATT (Seq. ID No. 81); GAA-ATT-TCC-TGT-TGA-CAG-A (Seq. ID No. 82); GTT-TGA-AAG-CTG-AAC-TAT-G (Seq. ID No. 83); TCC-TGT-AAT-GTT-CGA-CAG (Seq. ID No. 84); TCA-TAG-AAC-GCT-AGA-AAG (Seq. ID No. 85); ACC-TTT-CTT-TTG-ATG-AAG-GA (Seq. ID No. 86); CAA-ATA-TCA-CAA-AAA-GAG-GG (Seq. ID No. 87); GAG-TTG-AAT-AGA-GGC-AAC (Seq. ID No. 88); GGC-CAA-ATG-TAG-AAA-AGG (Seq. ID No. 89); GCG-TTC-AAC-TCA-AGG-TGT (Seq. ID No. 90); TGT-CCT-TTA-GAC-AGA-GCA (Seq. ID No. 91); TGA-GAC-CAA-ATG-TAC-AAA-AG (Seq. ID No. 92); GAA-TAC-TGA-GTA-AGT-TCT-TTG (Seq. ID No. 93); AAC-TGC-ACA-AAT-AGG-GTG (Seq. ID No. 94); TGG-AGA-CAC-TGT-GTT-TGT (Seq. ID No. 95); CCA-GTT-GGA-GAT-TTC-AAT (Seq. ID No. 96); GAA-GCC-TGC-CAG-TGG-ATA (Seq. ID No. 97); TAC-AGC-ATT-CTG-GAA-ACC (Seq. ID No. 98); CCA-GAC-ACT-GCG-TAG-TGA (Seq. ID No. 99); ATA-TAA-TGC-TAG-AGG-GAG (Seq. ID No. 100); AAA-AAC-AAG-ACA-AAC-TCG (Seq. ID No. 101); ATT-TCA-GCT-GAC-TAA-ACA (Seq. ID No. 102); AAC-GAA-TTA-TGG-TCA-CAT (Seq. ID No. 103); GGT-GAC-GAC-TGA-GTT-TAA (Seq. ID No. 104); TTT-GGA-CCA-CTC-TGT-GGC (Seq. ID No. 105); AAC-GGG-ATA-ACT-GCA-CCT (Seq. ID No. 106); TTT-GTG-GTT-TGT-GGT-GGA (Seq. ID No. 107); AGG-GAA-TAG-CTT-CAT-AGA (Seq. ID No. 108); ATC-ACG-AAG-AAG-GTT-CTG (Seq. ID No. 109); CCG-AAG-ATG-TCT-TTG-GAA (Seq. ID No. 110); AAA-GAG-GTC-TAC-ATG-

TCC (Seq. ID No. 111); TTC-CCG-TAA-CAA-CTA-TGC (Seq. ID No. 112); TCC-CGT-AAC-AAC-TAG-GCA (Seq. ID No. 113); AAA-AGG-AGT-GAT-CCA-ACC (Seq. ID No. 114); TCC-CTT-TGG-TAG-AGC-AGG (Seq. ID No. 115); ATT-TGA-GAT-GTG-TGT-ACT-CA (Seq. ID No. 116); GCA-CTT-ACC-GGC-CTA-AG (Seq. ID No. 117) and CTC-AGA-AAC-TTA-CTC-GTG (Seq. ID No. 118).



*(iii) Remarks On The Amendment To The Claims:*

Applicant continues to traverse the restriction/election requirement.

Accordingly, no claims have been canceled and amendments have been made to pending claims other than merely claims 10-12.

Antecedent basis for amending “non-nucleic acid” to “PNA” in various claims can be found throughout the specification but in particular at page 14, lines 16-21.

Antecedent basis for adding the limitation “of 10 to 30 subunits in length” in various claims can be found throughout the specification but in particular at page 20, lines 6-9.

Antecedent basis for defining the formula of a PNA probe or PNA probes in various claims can be found throughout the specification but in particular at page 14, lines 22-27 wherein it is specifically stated: “including any of the polymers referred to or claimed as peptide nucleic acids in ... and 5,986,053; all of which are herein incorporated by reference.” The formula for a PNA now inserted into the claims can be found in US 5,986,053 at col. 5, line 10 to col. 6, line 48, provided however that certain of the recited elements/limitations have been deleted so that the PNA oligomer would not be considered a PNA/DNA chimera. Applicant submits that this is a well-established definition of a PNA oligomer; one that is supported in the claims of numerous issued US patents.

Antecedent basis for amending “and” to “and/or” in claim 10 can be found throughout the specification but in particular at page 30, lines 6-9 wherein it is clear that a set can be designed for one, two or more human chromosomes.

It is respectfully submitted that the amendment does not introduce new matter.



#### IV. RESPONSE TO THE OFFICE ACTION REJECTIONS

##### **Rejections Under 35 U.S.C. § 112, First Paragraph**

At paragraph 4 of the Office Action, the Examiner rejected claims 10-12 under 35 U.S.C. § 112, first paragraph. Generally, the Examiner argued that the specification did not enable the full scope of the claimed subject matter. The claims, as amended, are now limited to PNA probes of a defined length and defined structure; a well accepted structure for PNA. Accordingly, it is believed that the amendments render moot the articulate rejections of paragraph 4 of the Office Action. Thus, it is believed that this rejection should be withdrawn.

At paragraph 5 of the Office Action, the Examiner rejected claims 10-12 under 35 U.S.C. § 112, first paragraph. Generally, the Examiner reiterated much of the argument of paragraph 4 of the Office Action, arguing lack of possession as compared with lack of enablement, but in particular appears to argue that claim 10 is deficient because it is not limited to specific nucleobase sequences. Claim 10 has been amended as discussed above. However, Applicant further respectfully submits that the methods disclosed in the specification for generating sequences suitable for chromosome determination using PNA probes fully support the scope of the presently claimed subject matter and do not constitute undue experimentation. Accordingly it is believed that this rejection should properly be withdrawn.

##### **2. Rejection Under 35 U.S.C. § 102(b)**

###### *(a) Statement Of The Law Of 35 U.S.C. § 102(b)*

It is well settled that to be anticipated, a prior art reference must teach each and every element/limitation of the claimed subject matter. M.P.E.P. § 2131. Moreover, the elements must be arranged as required by the claim. *Id.* "The identical invention must be shown in as complete detail as is contained in the claim" *Id.* quoting from *Richardson v. Suzuki Motor Co.*, 868 F2d 1226, 1236, 9 USPQ2d 1913, 1920 (Fed. Cir. 1989).

###### *(b) The Rejection*

At paragraph 7 of the present Office Action the Examiner rejected claims 10 and 11 under 35 U.S.C. § 102(a) and § 102(e) as being anticipated by Hyldig-Nielsen et al. (US 5,985,563). It is respectfully submitted that the present amendments render moot

the articulated rejection. Accordingly, it is believed that the rejection should be withdrawn.

#### V. SUMMARY

It is believed that this response addresses all rejections set forth in the present Office Action and the application is in ready condition for allowance. In consideration of the preceding amendments and remarks, Applicant hereby respectfully requests reconsideration of all pending claims (as amended), the withdrawal of all rejections set forth in the present Office Action and issue of a Notice of Allowance by The Office.

#### VI. INTERVIEW

If the Examiner believes a telephonic or personal interview would advance the prosecution of the subject application, the Examiner is invited to contact attorney Gildea during business hours at the telephone or facsimile numbers listed below.

#### VII. FEES

The petition under 37 C.F.R. §1.136(a) that accompanies this paper includes an authorization to deduct the appropriate fee from Deposit Account 02-3240. A supplemental IDS accompanies this paper and includes an authorization to deduct the appropriate fee from Deposit Account 02-3240. No additional fees are believed due The Office for consideration of this paper. If however, The Office determines that any other fee is due, authorization is hereby granted to charge any required fee associated with the filing or proper consideration of this paper to Deposit Account 02-3240.

#### VIII. CORRESPONDENCE/CUSTOMER NUMBER

Please send all correspondence pertaining to this document to:

Applied Biosystems  
Attn: Brian D. Gildea, Esq.  
15 DeAngelo Drive  
Bedford, MA 01730  
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Respectfully submitted  
on behalf of Applicant,

Oct 9, 2003

Date

Brian D. Gildea

Brian D. Gildea, Esq.

Reg. No. 39,995